

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:52:32 ; Search time 40.56 Seconds
(without alignments)
4.088 Million cell updates/sec

Title: US-08-833-506C-120

Perfect score: 33

Sequence: 1 QGILERV 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 76368

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : A.Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	9	W81272	Human INOS peptide
2	33	100.0	9	W81273	Human INOS peptide
3	33	100.0	12	W81238	Human INOS peptide
4	33	100.0	12	W81301	Human INOS peptide
5	33	100.0	14	W81237	Human INOS peptide
6	33	100.0	14	W81300	Human INOS peptide
7	33	100.0	15	W81233	Human INOS peptide
8	33	100.0	15	W81296	Human INOS peptide
9	29	87.9	8	W81274	Human INOS peptide
10	24	72.7	9	W81239	Human INOS peptide
11	24	72.7	9	W81302	Human INOS peptide
12	23	69.7	9	P33522	Amino acid sequenc
13	23	69.7	10	R33352	Sequence of trypti
14	23	69.7	15	W95122	Peptide K9 express
15	22	66.7	12	W81234	Human INOS peptide
16	22	66.7	12	W81297	Human INOS peptide
17	21	63.6	8	P33513	Amino acid sequenc
18	21	63.6	9	W49676	Human leucocyte an
19	21	63.6	13	P33520	Amino acid sequenc
20	21	63.6	15	W59086	FMDV non-structura
21	20	60.6	5	R62202	CENP-B protein ami
22	20	60.6	7	W66560	Peptide useful as
23	20	60.6	8	R73345	Human TSH receptor
24	20	60.6	8	R73347	Human TSH receptor
25	20	60.6	11	R77218	Mouse anti-human I
26	20	60.6	14	R65049	Random biotinylati
27	20	60.6	14	W11550	FGF9 antigenic pep
28	20	60.6	14	W46652	Biotinylation pep
29	20	60.6	15	P90253	Antigenic peptide
30	19	57.6	4	W46528	Peptide containing
31	19	57.6	6	W87171	Peptide determined
32	19	57.6	7	R71398	VPI peptide used t
33	19	57.6	7	W38293	Poliovirus amino a
34	19	57.6	8	P51212	Analgesic peptide.

35	19	57.6	8	1	R61079	Dynorphin-like pol
36	19	57.6	9	1	R61086	Dynorphin-like pol
37	19	57.6	9	1	R61878	MBP peptide 145, p
38	19	57.6	9	1	R61674	HLA-A2.1 algorithm
39	19	57.6	9	1	R73694	Antigen fragment 1
40	19	57.6	9	1	W01521	Amine-functional
41	19	57.6	11	1	R54763	Plasminogen analog
42	19	57.6	11	1	R61961	MBP peptide 143, p
43	19	57.6	11	1	R67619	Joba fatty acyl-
44	19	57.6	13	1	W93441	Staphylococcus aur
45	19	57.6	13	1	W94981	MHC binding peptid
46	19	57.6	14	1	R89867	Cytochrome P450 2C
47	19	57.6	14	1	W64077	Human cytochrome p
48	19	57.6	15	1	R44125	Human myelin basic
49	19	57.6	15	1	R65066	Random biotinylati
50	19	57.6	15	1	R35373	Residues 146-160 o
51	19	57.6	15	1	W05721	Residues 148-162 o
52	19	57.6	15	1	W54678	Peptide from MBP 1
53	19	57.6	15	1	W68579	P. carinii serine
54	19	57.6	15	1	W73606	Human myelin basic
55	18	54.5	6	1	R45221	des-Tyr Dynorphin
56	18	54.5	6	1	R88613	RGD hexapeptide. N
57	18	54.5	6	1	W65973	Dynorphin A (resid
58	18	54.5	7	1	R45210	des-Tyr Dynorphin
59	18	54.5	7	1	R45220	des-Tyr Dynorphin
60	18	54.5	7	1	R91345	Dynorphin A analog
61	18	54.5	7	1	R31336	Dynorphin A analog
62	18	54.5	7	1	W65963	Des-Tyr dynorphin
63	18	54.5	7	1	W65972	Des-Tyr-Gly dynorp
64	18	54.5	7	1	W66555	Peptide useful as
65	18	54.5	7	1	W96295	Vgab peptide fragm
66	18	54.5	8	1	P71269	Sequence of new an
67	18	54.5	8	1	P40299	Proenkephalin, the
68	18	54.5	8	1	P20254	Opitoid peptide 2.
69	18	54.5	8	1	R42485	Peptide 3 from neu
70	18	54.5	8	1	R45209	des-Tyr Dynorphin
71	18	54.5	8	1	R45219	des-Tyr Dynorphin
72	18	54.5	8	1	R60463	Antiproliferative
73	18	54.5	8	1	R61022	Dynorphin-like pol
74	18	54.5	8	1	R38769	Dynorphin-like pol
75	18	54.5	8	1	R61726	PLP peptide 131, p
76	18	54.5	8	1	R61751	MBP peptide 34, po
77	18	54.5	8	1	R91344	Dynorphin A analog
78	18	54.5	8	1	R91335	Dynorphin A analog
79	18	54.5	8	1	W50080	Human chorionic go
80	18	54.5	8	1	W50045	Human beta-hcg pro
81	18	54.5	8	1	W47485	Des-Tyr dynorphin
82	18	54.5	8	1	W65962	Des-Tyr-Gly dynorp
83	18	54.5	8	1	W65971	Peptide useful as
84	18	54.5	8	1	W65556	E. coli uracil DNA
85	18	54.5	9	1	R74446	ANP receptor agon1
86	18	54.5	9	1	R27447	ANP receptor agon1
87	18	54.5	9	1	R27447	ANP receptor agon1
88	18	54.5	9	1	R27453	ANP receptor agon1
89	18	54.5	9	1	R27454	ANP receptor agon1
90	18	54.5	9	1	R45208	des-Tyr Dynorphin
91	18	54.5	9	1	R45218	des-Tyr Dynorphin
92	18	54.5	9	1	R61088	Dynorphin-like pol
93	18	54.5	9	1	R61816	PLP peptide 134, p
94	18	54.5	9	1	R73827	Antigen fragment 1
95	18	54.5	9	1	R73819	Antigen fragment 1
96	18	54.5	9	1	R73820	Antigen fragment 1
97	18	54.5	9	1	R73100	Antigen fragment 1
98	18	54.5	9	1	R78913	MAGE 1 38-46 cyt
99	18	54.5	9	1	R91343	Dynorphin A analog
100	18	54.5	9	1	W60481	Tumour homing pept

ALIGNMENTS

RESULT 1
W81272

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ID W81272 standard; peptide; 9 AA.
AC W81272; 1999 (first entry)
DE Human iNOS peptide fragment PS-5275.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9
FT FT /note= "Val residue amidated"
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 13; Page 55; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 9 AA;

Query Match 100.0%; Score 33; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILERV 7
Db 3 QGILERV 9

RESULT 3
W81238
ID W81238 standard; peptide; 12 AA.
AC W81238; 1999 (first entry)
DE Human iNOS peptide fragment PS-5227.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 12
FT FT /note= "Val residue amidated"
PN WO9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 37; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 12 AA;

Query Match 100.0%; Score 33; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILERV 7
Db 5 QGILERV 11

RESULT 4
W81301
ID W81301 standard; peptide; 12 AA.
AC W81301;

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DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment for epitope mapping #22.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN WO9845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7C; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 12 AA;
 SQ Sequence 12 AA;

 Query Match 100.0%; Score 33; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

 QY 1 QGILERV 7
 Db 5 QGILERV 11
 |||||

 RESULT 5
 ID W81237 standard; peptide; 14 AA.
 AC W81237;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5226.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified_site 14 /note= "Gly residue amidated"
 FT
 PN WO9845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Page 37; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following

CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 14 AA;
 SQ Sequence 14 AA;

 Query Match 100.0%; Score 33; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

 QY 1 QGILERV 7
 Db 5 QGILERV 11
 |||||

 RESULT 6
 ID W81300 standard; peptide; 14 AA.
 AC W81300;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment for epitope mapping #21.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN WO9845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7C; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 14 AA;
 SQ Sequence 14 AA;

 Query Match 100.0%; Score 33; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0;

 QY 1 QGILERV 7
 Db 5 QGILERV 11
 |||||

 RESULT 7
 ID W81233 standard; peptide; 15 AA.
 AC W81233;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5222.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers

PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R.
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Page 37; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention.
 SQ Sequence 9 AA;

Query Match 72.7%; Score 24; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGILE 5
 |||||
 Db 5 OGILE 9

RESULT 11

W81302
 ID W81302 standard; peptide; 9 AA.
 AC W81302;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment for epitope mapping #23.
 DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R.
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7C; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention.
 SQ Sequence 9 AA;

Query Match 72.7%; Score 24; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGILE 5
 |||||

Db 5 OGILE 9

RESULT 12

P93522
 ID P93522 standard; protein; 9 AA.
 AC P93522;
 DT 03-JUN-1990 (first entry)
 DE Amino acid sequence of polylinker region of transfer vector pBF129
 DE Polylinker protein; silkworm nuclear polyhedrosis virus; NPV;
 KW HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF129.
 PN J01074990-A.
 PD 20-MAR-1989.
 PF 17-SEP-1987; 231107.
 PR 17-SEP-1987; JP-231107.
 PA (MAED) Maeda S.
 PI WPI: 89-127530/17.
 DR N-PSDB; N92398.
 PT New transfer vector pBFs, for HIV diagnosis -
 PT contg. promoter region of polyhedrin protein gene for silkworm
 PT nuclear polyhedrosis virus deoxyribonucleic acid
 PS Figure 2; page 9; 11pp; Japanese.
 CC Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin
 CC protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined
 CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region
 CC of the vector. Thus, HIV antigenic protein can be produced in large
 CC ams. and used as an antigen for the diagnosis of HIV or for
 CC vaccine production.
 SQ Sequence 9 AA;

Query Match 69.7%; Score 23; DB 1; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.5e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGILER 6
 :|||:
 Db 3 EGILDR 8

RESULT 13

R33352
 ID R33352 standard; peptide; 10 AA.
 AC R33352;
 DT 30-JUN-1993 (first entry)
 DE Sequence of tryptic peptide derived from purine-rich repeat (GA
 DE repeat) binding protein (GABP) at peale 1.
 KW GA binding protein; cis-regulatory element; VP16 mediated induction.
 OS Synthetic.
 PN W09304166-A.
 PD 04-MAR-1993.
 PF 17-AUG-1991; U06748.
 PR 16-AUG-1991; US-746032.
 PA (CARN-) CARNEGIE INST WASHINGTON.
 PI Lamarco KL, Mc Knight SL, Thompson CC;
 DR WPI: 93-093998/11.
 PT DNA encoding GA binding protein sub-unit - allows investigation
 PT of sub-unit sequence motif functions, for control of rapid cell
 PT division e.g. in cancer
 PS Disclosure; Page 3; 68pp; English.
 CC A cis-regulatory element required for virion associated protein VP16
 CC mediated induction of herpes simplex virus 1 (HSV1) immediate early
 CC (IE) genes consists of three imperfect repeats of the purine-rich
 CC hexanucleotide 5'-CGGAAR-3'. A protein complex capable of avid
 CC interaction with the purine-rich repeats (GA repeats) has been
 CC identified in soluble preparations of rat liver nuclei. This GA
 CC binding protein (GABP) consists of two separable subunits.
 CC Applicants have isolated cDNA clones encoding both subunits of GABP
 CC and have revealed that one (GABP alpha) is related to the Ets
 CC transforming protein, while the other (GABP beta) contains a
 CC series of 33-amino acid repeats related in sequence to a variety
 CC of proteins.

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SQ Sequence 10 AA;
Query Match 69.7%; Score 23; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILER 6
Db 5 QGVIEK 10

RESULT 14
W5122
ID W5122 standard; peptide; 15 AA.
AC W5122;
DT 24-MAY-1999 (first entry)
DE Peptide K9 expressed by a modified bacteriophage library.
KW Modified phage library; screening; cell-surface associated protein;
KW therapeutic; diagnostic; disease; ligand; drug; toxin; fractionation;
KW noise elimination; bacteriophage.
OS Bacteriophage ml3.
PN W09906542-A1.
PD 11-FEB-1999.
PF 29-JUL-1998; G02269.
PR 30-JUL-1997; GB-016094.
PA (UNIU ) UNIV GLASGOW.
PI Allen JM, Lavery E;
DR WPI; 99-153772/13.
PT Modified phage display library depleted in phage that react with
PT native cellular proteins - provides reduced noise and higher
PT signal-to-noise ratio when screened against cells transfected to
PT express a specific heterologous protein, used to identify potential
PT therapeutic and diagnostic agents
PS Example 1; Page 29; 49pp; English.
CC The invention relates to a modified phage library for use with a selected
CC strain of cells that have been transformed to express a heterologous
CC protein (I) in a screening procedure, to detect specific binding between
CC individual phage and a recognition site on the heterologous protein. The
CC modified library is produced as follows. The initial phage library is
CC fractionated by contact with strain of cells that do not express (I) to
CC bind any phage that bind to cellular proteins other than the (I). Bound
CC and unbound phages are separated to produce the modified library,
CC depleted in components that bind proteins other than (I). The library is
CC used to identify phage that bind to cell-surface associated (I),
CC specifically receptors. Peptides identified by screening with the
CC modified library are potentially useful as therapeutic and diagnostic
CC agents, for diseases involving (I) or its ligands (including as carriers
CC for delivering drugs, toxins or antibodies to cells), and their amino
CC acid sequences can be used to design other agents for the same uses. The
CC initial fractionation eliminates much of the noise caused by binding to
CC other cell-surface proteins, and the use of transfected cells for
CC screening (these express a far greater number of (I) than wild-type
CC cells) improves the signal-to-noise ratio. The number of rounds of
CC screening may thus be reduced.
SQ Sequence 15 AA;

Query Match 69.7%; Score 23; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERV 7
Db 2 GTLERV 7

RESULT 15
W81234
ID W81234 standard; peptide; 12 AA.
AC W81234;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5223.

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KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Location/Qualifiers
FT Modified_site 12 /note= "His residue amidated"
FT WO9845710-A1.
PN 15-OCT-1998.
PD 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI; 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 36; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 12 AA;
SQ Sequence 12 AA;

Query Match 66.7%; Score 22; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILERV 7
Db 1 ILERV 5

RESULT 16
W81297
ID W81297 standard; peptide; 12 AA.
AC W81297;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment for epitope mapping #18.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
OS Homo sapiens.
PN WO9845710-A1.
PD 15-OCT-1998.
PR 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI; 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Fig 7B; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence

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CC represents a peptide from human INOS which is used in the method of the
 CC invention.
 SQ Sequence 12 AA;

Query Match 66.7%; Score 22; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILERV 7

||||

Db 1 ILERV 5

RESULT 17

P93513

ID P93513 standard; protein; 8 AA.

AC P93513;

DT 03-JUN-1990 (first entry)

DE Amino acid sequence of polylinker region of transfer vector pBF5

KW Polylinker protein; silk worm nuclear polyhedrosis virus; NPV;

KW HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF5.

PN J01074990-A.

PD 20-MAR-1989.

PF 17-SEP-1987; 231107.

PR 17-SEP-1987; JP-231107.

PA (MAED) Maeda S.

PI WPI; 89-127530/17.

DR N-PSDB; N92389.

PT New transfer vector pBFs, for HIV diagnosis -

PT contg. promoter region of polyhedrin protein gene for slink-worm

PT nuclear polyhedrosis virus deoxyribonucleic acid

PS Figure 2; page 9; 11pp; Japanese.

CC Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin

CC protein gene of silk worm nuclear polyhedrosis virus (NPV) recombined

CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region

CC of the vector. Thus, HIV antigenic protein can be produced in large

CC ams. and used as an antigen for the diagnosis of HIV or for

CC vaccine production.

CC Sequence 8 AA;

SQ

Query Match

63.6%; Score 21; DB 1; Length 8;

Best Local Similarity 80.0%; Pred. No. 1.5e+05;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILRV 6

||||

Db 3 GILDR 7

RESULT 18

W49676

ID W49676 standard; peptide; 9 AA.

AC W49676;

DT 05-JUN-1998 (first entry)

DE Human leucocyte antigen DQ4 binding peptide #567.

KW Human leucocyte antigen; HLA-DQ4; combinatorial library; allergy;

KW autoimmune disease.

OS Synthetic.

PN J08151396-A.

PD 11-JUN-1996.

PF 28-NOV-1994; 292657.

PR 28-NOV-1994; JP-292657.

PA (TEIJ) TEIJIN LTD.

PI WPI; 96-329479/33.

PT HLA-binding oligopeptide and an immuno-regulator contg it - used in

PT the treatment of autoimmune disease

PS Claim 5; Page 59; 61pp; Japanese.

CC This peptide is an example of a peptide which binds to a human leucocyte

CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid

CC combinatorial library comprising the sequence V05953, by screening with

CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune
 CC disease, especially for treatment of allergies.
 SQ Sequence 9 AA;

Query Match

63.6%; Score 21; DB 1; Length 9;

Best Local Similarity 50.0%; Pred. No. 1.5e+05;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILERV 7

||||

Db 1 GVLDR 6

RESULT 19

P93520

ID P93520 standard; protein; 13 AA.

AC P93520;

DT 03-JUN-1990 (first entry)

DE Amino acid sequence of polylinker region of transfer vector pBF81

KW Polylinker protein; silk worm nuclear polyhedrosis virus; NPV;

KW HIV gene; gag; pol; SOR; gp120; gp41; polylinker region; pBF81.

PN J01074990-A.

PD 20-MAR-1989.

PF 17-SEP-1987; 231107.

PR 17-SEP-1987; JP-231107.

PA (MAED) Maeda S.

PI WPI; 89-127530/17.

DR N-PSDB; N92396.

PT New transfer vector pBFs, for HIV diagnosis -

PT contg. promoter region of polyhedrin protein gene for slink-worm

PT nuclear polyhedrosis virus deoxyribonucleic acid

PS Figure 2; page 9; 11pp; Japanese.

CC Transfer vectors pBFs were prepd. contg. promoter region of polyhedrin

CC protein gene of silk worm nuclear polyhedrosis virus (NPV) recombined

CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region

CC of the vector. Thus, HIV antigenic protein can be produced in large

CC ams. and used as an antigen for the diagnosis of HIV or for

CC vaccine production.

CC Sequence 13 AA;

SQ

Query Match

63.6%; Score 21; DB 1; Length 13;

Best Local Similarity 80.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILRV 6

||||

Db 8 GILDR 12

RESULT 20

W59086

ID W59086 standard; peptide; 15 AA.

AC W59086;

DT 10-AUG-1998 (first entry)

DE FMDV non-structural viral protein immunogenic peptide fragment #14.

KW Foot and Mouth disease; FMDV; immunogenic; viral nonstructural protein;

KW immunoreactive; antibody; T cell; vaccine; pig; cattle.

OS Bos taurus.

PN DE19638044-A1.

PD 19-MAR-1998.

PF 18-SEP-1996; 038044.

PR 18-SEP-1996; DE-038044.

PA (FARB) BAYER AG.

PI Correa R, Froehlich B, Glatthaar-Saalmueller B, Hennen H,

PI Pauly T, Pfaffe E, Saalmueller A, Wiesmueller K;

DR WPI; 98-180328/17.

PT Vaccines against foot and mouth disease virus - comprising peptide

PT fragments of nonstructural viral proteins

PS Claim 1; Page 14; 27pp; German.

CC W59073-W59119 are immunogenic peptides from a foot and mouth disease

CC virus (FMDV) nonstructural protein which are immunoreactive with
 CC FMDV-specific antibodies or T cells and can be used in vaccines
 CC against the disease. The vaccines are used especially for immunising
 CC pigs and cattle.
 SQ Sequence 15 AA;

Query Match 63.6%; Score 21; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILER 6
 DB 9 GILER 13

RESULT 21
 R62202 ID R62202 standard; Protein; 5 AA.
 AC R62202; 03-MAY-1995 (first entry)
 DE CNP-B protein amino acids 473-477, homologous to HSV-1 IE motif.
 KW CNP-B protein; centromere protein; epitope;
 KW autoantibody; immunoinfective cluster virus; nuclear protein antigen;
 KW systemic rheumatic disorder; herpes simplex virus; HSV-1 IE;
 KW immediate early protein; systemic lupus erythematosus; scleroderma.
 OS Homo sapiens.
 PN WO9420141-A.
 PD 15-SEP-1994.
 PF 10-MAR-1994; U02631.
 PR 11-MAR-1993; US-029850.
 PA (UISC-) UNIV SOUTHERN CALIFORNIA.
 PI Douvas A, Ehresmann G, Takehana Y;
 DR Methods for treating immunoinfective cluster virus infections -
 PT utilise antibodies or fragments characteristic of auto antibodies
 PT produced by patients with rheumatic disorders
 PS Disclosure; Page 73; 106pp; English.
 CC A comparison of the CNP-B centromere protein sequence with proteins
 CC from immunoinfective cluster viruses revealed widespread
 CC homologies. The importance of these homologous motifs is that they
 CC are epitopes for autoantibodies occurring in high titres in systemic
 CC rheumatic disorders. Sera from such patients could be used for
 CC treatment of immunoinfective cluster virus infections, e.g. HIV-1,
 CC immunoinfective adenoviruses, human lymphotropic retroviruses,
 CC rubella virus, CMV and EBV infections.
 SQ Sequence 5 AA;

Query Match 60.6%; Score 20; DB 1; Length 5;
 Best Local Similarity 60.0%; Pred. No. 1.5e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5
 DB 1 QGVVE 5

RESULT 22
 W65560 ID W65560 standard; peptide; 7 AA.
 AC W65560;
 DT 26-NOV-1998 (first entry)
 DE Peptide useful as angiogenesis inhibitor.
 KW anti-angiogenic drug; cancer; arthritis; retinopathy; angiogenesis;
 KW inhibitor; cancer; arthritis; eye disease; macular degeneration;
 KW retinopathy.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified_site 1
 FT Misc_difference 3 /note= "Optional N-terminal acetyl"
 FT /note= "D-form residue"

FT Modified_site 7 /note= "Optionally Arg-NH2 or Arg-NHCH2CH3"
 FT WO9841542-A1.
 PN 24-SEP-1998.
 PD 16-MAR-1998; U05327.
 PR 17-MAR-1997; US-820667.
 PA (ABBO) ABBOTT LAB.
 PA (NOUN) UNIV NORTHWESTERN.
 PI Bouck NP, Dawson DW, Henkin J, Schneider AJ;
 DR WPI; 98-521165/44.
 PT New peptide(s) containing D-amino acid residues as angiogenesis
 PT inhibitors - for treatment of e.g. cancer, arthritis, eye diseases
 PS Example 42; Page 35; 57pp; English.
 CC The invention relates to peptides of formulae (I)-(IV): T-Gly-Val-D-Ile-
 CC Thr-Arg-Ile-U (I), V-Gly-D-Val-Ile-D-Thr-D-Arg-D-Ile-W (II), X-D-Arg-D-
 CC Ile-D-Arg-D-Thr-Ile-D-Val-Y (III), Z-Gly-Val-Ile-Thr-Arg-Ile-U, (IV). T
 CC is absent or is an N-protecting group or 1-12 amino acids, optionally
 CC terminated by an N-protecting group; U = Arg or Arg-NR1R2; R1 and R2 =
 CC hydrogen and 1-4C alkyl; V and X are absent or N-protecting groups.
 CC W = D-Arg or D-Arg-NR1R2; Y = Gly or Gly-NR1R2; Z = 1-12 amino acids,
 CC optionally terminated by a protecting group and including at least one
 CC D-amino acid. The peptides are inhibitors of angiogenesis (they inhibit
 CC migration of endothelial cells) and are useful for treatment of cancer,
 CC arthritis, psoriasis, infections of, or surgical injury to, the eye,
 CC macular degeneration or diabetic retinopathy. They can also be used
 CC for treating other autoimmune or ocular diseases, blood vessel disease,
 CC angiofibroma, wound granulation, etc. The present sequence represents an
 CC example of an angiogenesis inhibitor disclosed in the specification.
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1.5e+05;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILERV 7
 DB 1 GVIKRI 6

RESULT 23
 R73346 ID R73346 standard; Peptide; 8 AA.
 AC R73346;
 DT 12-DEC-1995 (first entry)
 DE Human TSH receptor (residues 291-298).
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;
 KW antibody; affinity; detection.
 OS Synthetic.
 PN J07089991-A.
 PD 04-APR-1995.
 PF 28-SEP-1993; 240853.
 PR 28-SEP-1993; JP-240853.
 PA (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
 DR WPI; 95-167251/22.
 PT Novel polypeptide(s) having affinity for the human TSH receptor
 PT antibody - used in detection of the TSH antibody.
 PS Example 1; Page 25; 54pp; Japanese.
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC R73201-592).
 SQ Sequence 8 AA;

Query Match 60.6%; Score 20; DB 1; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5
 DB 3 RGILE 7

RESULT 24

R73347 ID R73347 standard; Peptide; 8 AA.
 AC R73347;
 DT 12-DEC-1995 (first entry)
 DE Human TSH receptor (residues 293-300).
 KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;
 KW antibody; affinity; detection.
 OS Synthetic.
 PN J07089991-A.
 PD 04-APR-1995.
 PR 28-SEP-1993; 240853.
 PR 28-SEP-1993; JP-240853.
 PA (MITP) MITSUBISHI PETROCHEMICAL CO LTD.
 DR WPI; 95-167251/22.
 PT Novel polypeptide(s) having affinity for the human TSH receptor
 PT antibody - used in detection of the TSH antibody.
 PS Example 1; Page 25; 54pp; Japanese.
 CC Peptides with affinity to human TSH (thyroid stimulating hormone)
 CC receptor antibody are used for detection of the antibody. (See also
 CC R73201-592)
 SQ Sequence 8 AA;

Query Match 60.6%; Score 20; DB 1; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5

Db :|||
 1 RGILE 5

RESULT 25

R77218 ID R77218 standard; Peptide; 11 AA.

AC R77218;
 DT 23-AUG-1995 (first entry)
 DE Mouse anti-human IL-6 Ab H chain V region framework region 4.
 KW Primer; PCR; amplification; kappa; light chain; variable region; mouse; human;
 KW Interleukin; antibody; hybridoma; CDR; framework; constant region;
 KW heavy chain; disorder; antigenicity.
 OS Synthetic.
 PN W09428159-A.
 PD 08-DEC-1994.
 PR 30-MAY-1994; J00859.
 PR 31-MAY-1993; JP-129787.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PI Hirata Y, Sato K, Tsuchiya M;
 DR WPI; 95-022828/03.
 PT Antibody against IL-6 - useful for the therapy and treatment of
 PT IL-6 related disorders.
 PS Claim 13; Page 66; 82pp; Japanese.

CC The sequence of the mouse anti-human interleukin-6 (IL-6) antibody heavy
 CC chain variable region framework region (FR) 4. The sequences of FR1-4
 CC (R77215-8) were used in conjunction with the complementarity determining
 CC regions 1-3 (R77212-4) to construct a chimaeric antibody against human
 CC interleukin-6 (IL-6). The vectors Q75914-7 express constructs encoding
 CC fragments of a chimaeric antibody to the human IL-6 comprising (a) a
 CC light chain with (i) a variable region containing 3 CDR (R77201-3)
 CC inserted into several framework regions (FR) (R77204-7) and (ii) a human
 CC light chain constant region and (b) a heavy chain with (i) a variable
 CC region containing 3 CDR (R77212-4) inserted into FR (R77215-8) and (ii)
 CC a human light chain constant region. The FR of the light chain may be
 CC mouse derived (Q75888) or from the human antibody REI. The heavy chain
 CC FR may also be mouse derived (Q75889) or from the human antibody DAW.
 CC The antibodies can be used in the treatment of IL-6 related disorders.
 CC The antibodies are useful as they have low antigenicity due to the use of
 CC human derived sequences and low antigenicity mouse derived sequences.
 SQ Sequence 11 AA;

Query Match 60.6%; Score 20; DB 1; Length 11;
 Best Local Similarity 71.4%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILERV 7

Db :|||
 3 QGILVTV 9

RESULT 26

R65049 ID R65049 standard; Peptide; 14 AA.

AC R65049;
 DT 24-OCT-1995 (first entry)
 DE Random biotinylation peptide 17.
 KW biotinylation; peptide; recombinant; fusion protein; small;
 KW specific; defined; purification; BirA; enzyme; biotin.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_site 9 /note= "biotin-Lys"
 PN W09504069-A.
 PD 09-FEB-1995.

PR 28-JUL-1994; U08528.
 PR 30-JUL-1993; US-095991.

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PI Schatz PJ;
 DR WPI; 95-090609/12.

PT Production of biotinylated proteins by expression of a
 PT recombinant DNA vector - which encodes a fusion protein
 PT comprising a protein and a biotinylated peptide.
 PS Claim 10; Page 136; 146pp; English.
 CC A library of small, efficient peptide biotinylation sequences (R65048-66)
 CC was generated by using a generic peptide (R65047) and a system known as
 CC the "peptides on plasmids" system. At some positions in the sequences,
 CC no clear consensus is apparent. At other residues, however, clear trends
 CC emerge. A protein can be biotinylated by constructing a recombinant DNA
 CC expression vector encoding a fusion protein, comprising a protein and a
 CC biotinylation peptide. A host cell, eg. E. coli is transformed with the
 CC vector and is cultured in the presence of biotin and a biotinylation
 CC enzyme, eg. BirA.
 SQ Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QGILE 5

Db :|||
 2 QGIFE 6

RESULT 27

W11550 ID W11550 standard; Peptide; 14 AA.

AC W11550;
 DT 19-SEP-1997 (first entry)
 DE FGF9 antigenic peptide, Sp32.
 KW Mouse; chicken; fibroblast growth factor 9; FGF9; detection;
 KW fibroblast growth factor receptor 3; FGFR3; cartilage repair;
 KW bone repair; antagonist; anti-FGF9 antibody; endochondromas;
 KW solitary hereditary exostosis; multiple hereditary exostosis;
 KW hallux valgus deformity; achondroplasia; synovial chondromatosis.
 OS Synthetic.
 PN W09641523-A1.
 PD 27-DEC-1996.
 PR 12-JUN-1996; IL0011.
 PR 12-JUN-1995; US-000137.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Yayon A;
 DR WPI; 97-065215/06.
 PT Medical and diagnostic use of fibroblast growth factor 9 - and

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PT recombinant fibroblast growth factor 9 DNA
PS Example 1; Page 7; 32pp; English.
CC The sequences given in W11549-50 represent antigenic peptide fragments
CC of fibroblast growth factor 9 (FGF9) which were used in the production
CC of anti-FGF9 antibodies. FGF9 is used in the method of the invention
CC for detecting fibroblast growth factor receptor 3 (FGFR3) in a sample
CC or tissue. The method comprises contacting the sample or tissue with
CC FGF9, allowing formation of receptor-ligand pairs, and detecting any
CC FGFR3-FGF9 pairs. Compositions containing FGF9 can be used to increase
CC FGFR3 activity, esp. to stimulate cartilage or bone repair. Compositions
CC containing FGF9 antagonists or FGF9 binding agents (e.g. anti-FGF9
CC antibodies) can be used to treat diseases caused by an excess of FGF9
CC or overactivity of FGFR3, esp. multiple or solitary hereditary exostosis,
CC hallux valgus deformity, achondroplasia, synovial chondromatosis and
CC endochondromas.
SQ Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OGILER 6
Db 4 KGILRR 9

RESULT 28
W46652
ID W46652 standard; peptide; 14 AA.
AC W46652;
DE 28-MAY-1998 (first entry)
DT Biotinylation peptide isolated from random library 2.
DW Biotinylation peptide; biotinylation enzyme; biotin-protein ligase;
KW BIRA; biotin ligase; biotin; purification; immobilisation; labelling;
KW detection; protein.
OS Synthetic.
PN US5723584-A.
PD 03-MAR-1998.
PF 03-FEB-1995; 383753.
PR 30-JUL-1993; US-099991.
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
PI Schatz PJ;
DR WPI; 98-178542/16.
PT Peptide(s) that can be biotinylated by biotin ligase - and fusion
PT proteins containing them
PS Claim 3; Column 66; 33pp; English.
CC Peptides W46651-69 are non-naturally occurring biotinylation peptides,
CC derived from a library constructed to express peptides of the generic
CC sequence W46650. The library was constructed using oligonucleotides
CC V16121-23. The peptides contain a biotinylatable sequence motif,
CC recognised by a biotinylation enzyme, e.g. biotin-protein ligase (BIRA).
CC The C or N terminus of the peptides can be covalently coupled to a
CC protein that is incapable of being biotinylated by a biotin ligase.
CC The peptides can be biotinylated in vitro or in vivo, especially with
CC BIRA biotin ligase, and used for the purification, immobilisation,
CC labelling or detection of proteins.
SQ Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OGILE 5
Db 2 QGIFE 6

RESULT 29
P90253
ID P90253 standard; peptide; 15 AA.
AC P90253;

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DT 26-FEB-1990 (first entry)
DE Antigenic peptide for detecting, inhibiting and neutralising HIV-1.
KW HIV-1; antigenic determinants.
OS HIV-1.
PN EP-330359-A.
PD 30-AUG-1989.
PF 14-FEB-1989; 301364.
PR 25-FEB-1988; US-160378.
PA (BIRA) Bio Rad Labs Inc.
PI Walker RP; Parekh BS;
DR WPI; 89-250452/35.
DT New peptide(s) for detecting, inhibiting and neutralising HIV-1
DT corres. to antigenic determinants encoded by conserved regions
DT of HIV-1 genome.
PS Disclosure; page 4; 16pp; English.
CC Peptide is one of several fragments from gp 120 and gp41 (env gene)
CC p18 and p24 (gag gene), p32 (pol gene) and proteins encoded by the
CC tat, orf trs/art and sor genes. They are used for detecting,
CC inhibiting and neutralising HIV-1 infection. Dosage is pref.
CC 5-25 mg/kg. The peptides can be used for any type of immunological
CC detection esp. dot blot and ELISA.
CC See also P90191-P90274.
SQ Sequence 15 AA;

Query Match 60.6%; Score 20; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5
Db 1 QGVVE 5

RESULT 30
W46528
ID W46528 standard; peptide; 4 AA.
AC W46528;
DE 20-MAY-1998 (first entry)
DT Peptide containing a protease binding site.
DW Protease binding site; protease; protease indicator; fluorescent signal;
KW detection; protease activity.
OS Synthetic.
PN US5714342-A.
PD 03-FEB-1998.
PF 27-OCT-1995; 549008.
PR 27-OCT-1995; US-549008.
PR 28-OCT-1994; US-331383.
PA (ONCO-) ONCOIMMUNIN INC.
PI Komoriya A, Packard BS;
DR WPI; 98-158345/14.
DT Fluorogenic substrates for protease determination - having two
DT closely spaced fluorophores flanking protease binding site
PS Disclosure; Column 4; 39pp; English.
CC Peptides W46520-53 contain protease binding sites. They are used to
CC produce novel reagents whose fluorescence increases in the presence of
CC particular proteases. These fluorogenic protease indicators (substrates)
CC provide a high intensity fluorescent signal at a visible wavelength when
CC they are digested by a protease. The fluorogenic indicators have the
CC general formula:
CC F1--C1--P--C2--F2
CC | |
CC (S1)n (S2)k
CC where:
CC P is a peptide containing a protease binding site, e.g. W46520-53.
CC F1 and F2 are fluorophores.
CC S1 and S2 are peptide spacers e.g. W46554-58.
CC n, k = 0 or 1.
CC C1 and C2 are conformation-determining regions that introduce a bend
CC into the composition which positions the fluorophores adjacent to each
CC other with a separation of less than 100 Angstrom.
CC When n is 1, S1 is joined to the terminal alpha-amino group of C1 by a
CC peptide bond, and when k is 1, S2 is joined to the terminal carboxy group

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CC of C2 by a peptide bond. The protease indicators are used for detecting
 CC protease activity in a biological sample. The sample is contacted with
 CC the indicator and any change in fluorescence is detected, an increase in
 CC fluorescence indicating protease activity.
 SQ Sequence 4 AA;

Query Match 57.6%; Score 19; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGIL 4
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 Db 1 OGIL 4

Search completed: June 30, 2000, 14:52:36
 Job time: 6003 sec

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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:54:15 ; Search time 50.08 seconds
(without alignments)
8.195 Million cell updates/sec

Title: US-08-833-506c-l20

Perfect score: 33

Sequence: 1 QCILERV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 2577

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

PIR_63:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	63.6	15	2 PA0076	fructose-bisphosph
2	19	57.6	14	2 S50900	chlorophyll a/b-bi
3	19	57.6	14	2 S35267	acetyl-CoA carboxy
4	18	54.5	9	2 PH0942	T-cell receptor be
5	18	54.5	15	2 A53085	lipid transfer pro
6	17	51.5	15	2 PS0382	Ig heavy chain J r
7	16	48.5	13	2 S09018	hemolytic protein
8	16	48.5	14	2 A59018	MUCL enhancer bind
9	15	45.5	10	2 S19296	16K protein - poul
10	15	45.5	13	2 I58003	hprt protein - Chi
11	15	45.5	14	2 S29789	hypothetical prote
12	15	45.5	14	2 S03530	Ig heavy chain J r
13	15	45.5	14	2 S65392	cytochrome-c oxida
14	15	45.5	15	2 PA0075	fructose-bisphosph
15	15	45.5	15	2 PA0102	fructose-bisphosph
16	15	45.5	15	2 PH1377	T antigen variant
17	14	42.4	7	2 PT0246	Ig heavy chain CRD
18	14	42.4	10	2 S06964	hypothetical prote
19	14	42.4	10	2 B56899	serum heterodimer,
20	14	42.4	11	1 XASNEA	bradykinin potenti
21	14	42.4	11	2 A61483	pyridoxal kinase (
22	14	42.4	11	2 S34065	ornithine decarbox
23	14	42.4	12	2 B58503	outer membrane por
24	14	42.4	12	2 C33099	148K exoantigen -
25	14	42.4	12	2 PH1467	T-cell receptor be
26	14	42.4	12	2 H41946	T-cell receptor ga
27	14	42.4	12	4 JX0315	aminotransferase c
28	14	42.4	13	2 S66235	sperm motility inh
29	14	42.4	14	2 S66234	sperm motility inh
30	14	42.4	14	2 C44823	synaptosomal-assoc

31	14	42.4	15	1 LFTWL	leu leader peptide
32	14	42.4	15	2 S21240	alpha-glucosidase
33	14	42.4	15	2 A28497	neurotensin-relate
34	14	42.4	15	2 D48394	major fat-globule
35	14	42.4	15	2 I40665	11vBN leader pepti
36	14	42.4	15	2 PN0629	integration host f
37	14	42.4	15	2 T09463	ribosomal protein
38	14	42.4	15	2 PA0071	superoxide dismuta
39	14	42.4	15	2 S05700	insulin-like growt
40	14	42.4	15	2 S05699	insulin-like growt
41	14	42.4	15	2 B56046	urinary tract ston
42	14	42.4	15	2 PH0806	T-cell receptor al
43	14	42.4	15	2 S17214	gap junction prote
44	13	39.4	4	2 E44823	synaptosomal-assoc
45	13	39.4	5	2 PT0278	Ig heavy chain CRD
46	13	39.4	8	2 T10077	hypothetical prote
47	13	39.4	10	2 JQ0943	hypothetical 1.3K
48	13	39.4	10	2 F44644	neurotoxin-associa
49	13	39.4	10	2 I44644	neurotoxin-associa
50	13	39.4	11	2 S70720	trigger factor hom
51	13	39.4	11	2 B41835	translation elonga
52	13	39.4	11	2 PH0903	T-cell receptor be
53	13	39.4	11	4 I54081	retinoic acid rece
54	13	39.4	12	2 B46662	collagen alpha 2(V
55	13	39.4	12	2 B56049	urinary tract ston
56	13	39.4	12	2 A42324	cytochrome P450c27
57	13	39.4	13	1 JZVHP1	crabrolin - Europe
58	13	39.4	13	2 S22889	1p9B protein - Shi
59	13	39.4	13	2 G44644	neurotoxin-associa
60	13	39.4	13	2 S14316	photosystem I 9K c
61	13	39.4	13	2 S09716	2S albumin large c
62	13	39.4	13	2 H44957	protein P18 - comm
63	13	39.4	13	2 S09019	hemolytic protein
64	13	39.4	13	2 A57789	gallbladder stone
65	13	39.4	14	2 JN0390	histamine-releasin
66	13	39.4	14	2 I54945	gene C protein - E
67	13	39.4	14	2 C39170	acyl-lacyl-carrier
68	13	39.4	14	2 PA0015	seed storage prote
69	13	39.4	14	2 A61306	ribonuclease M (EC
70	13	39.4	14	2 S58426	spermathecin AWN h
71	13	39.4	14	2 PH1639	Ig H chain V-D-J r
72	13	39.4	15	2 S26791	Ig heavy chain V r
73	13	39.4	15	2 A43298	myosin, gizzard -
74	13	39.4	15	2 S43321	RNA-binding protei
75	13	39.4	15	2 PQ0750	self-incompatibili
76	13	39.4	15	2 A61522	7.5k surfactant-as
77	13	39.4	15	2 F57789	gallbladder stone
78	13	39.4	15	2 B33527	fructose-2,6-bisph
79	13	39.4	15	2 S62675	collagen type I -
80	13	39.4	15	2 PH1590	Ig H chain V-D-J r
81	13	39.4	15	2 PT0096	pyruvate dehydroge
82	13	39.4	15	2 PH1455	T-cell receptor al
83	12	36.4	6	2 S11024	hydrogensulfite re
84	12	36.4	6	2 A49792	acylaminoacyl-pept
85	12	36.4	7	2 I54257	phenylalanine hydr
86	12	36.4	8	2 S20162	leghemoglobin III
87	12	36.4	8	2 A54823	olfactory receptor
88	12	36.4	8	2 B54823	olfactory receptor
89	12	36.4	9	2 A60427	macrophage cytotox
90	12	36.4	10	2 A60410	beta-neoendorphin
91	12	36.4	10	2 C38925	seed storage prote
92	12	36.4	10	2 PA0116	ferridoxin--NADP+
93	12	36.4	10	2 PS0220	ferridoxin--NADP+
94	12	36.4	10	2 S17048	cytochrome P450 (1
95	12	36.4	10	2 A61354	carnitine medium/1
96	12	36.4	10	2 S29190	kinase activator p
97	12	36.4	11	2 E41476	probable antigen 5
98	12	36.4	11	2 PC4267	ribosomal protein
99	12	36.4	11	2 PN0167	gene HEXA protein
100	12	36.4	12	2 I64829	

ALIGNMENTS

```

RESULT 1
PA0076
fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (Fusarium sporotrichioides) (fragm
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PA0076
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Reference number: PA0051
A:Accession: PA0076
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 63.6%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILER 6
   ||: ||
Db 5 QGLKER 10

RESULT 2
S50900
chlorophyll a/b-binding protein Lhcb5 - spinach (fragment)
N:Alternate names: light-harvesting complex LHCIIc protein
C:Species: Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C:Accession: S50900
R:Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A:Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclo
A:Reference number: S50900; MUID:95112835
A:Accession: S50900
A:Molecule type: protein
A:Residues: 1-14 <WAL>
C:Superfamily: chlorophyll a/b-binding protein
C:Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosys

Query Match 57.6%; Score 19; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILER 6
   ||: ||
Db 6 GLLDR 10

RESULT 3
S35267
acetyl-CoA carboxylase (EC 6.4.1.2) - wheat (fragment)
C:Species: Triticum aestivum (common wheat)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S35267
R:Gornicki, P.; Haselkorn, R.
Plant Mol. Biol. 22, 547-552, 1993
A:Title: Wheat acetyl-CoA carboxylase.
A:Reference number: S35267; MUID:93320392
A:Accession: S35267
A:Molecule type: protein
A:Residues: 1-14 <GOR>
A:Experimental source: leaf
C:Function:
A:Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A:Pathway: fatty acid biosynthesis
C:Keywords: fatty acid biosynthesis; ligase

Query Match 57.6%; Score 19; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 3.7e+02;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILERV 7
   ||::||
Db 4 KGVKKV 10

RESULT 4
PH0942
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0942
R:Gold, D.P.; Offner, H.; Sun, D.; Willey, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0941; MUID:92078857
A:Accession: PH0942
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the codon TGC for residue 2 as Ala
C:Keywords: T-cell receptor

Query Match 54.5%; Score 18; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5
   ||: ||
Db 3 KGLLE 7

RESULT 5
A53085
lipid transfer protein - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A53085
R:Ko, K.W.; Oikawa, K.; Ohnishi, T.; Kay, C.M.; Yokoyama, S.
Biochemistry 32, 6729-6736, 1993
A:Title: Purification, characterization, and conformational analysis of rabbit plasma
A:Reference number: A53085; MUID:93320050
A:Accession: A53085
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <ROL>
A:Experimental source: plasma
A:Note: sequence extracted from NCBI backbone (NCBIP:135263)

Query Match 54.5%; Score 18; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERV 7
   ||: ||
Db 10 GIVXRI 15

RESULT 6
PS0382
Ig heavy chain J region 2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 06-Jun-1997
C:Accession: PS0382
R:Lang, P.; Mocikat, R.
Gene 102, 261-264, 1991
A:Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse a
A:Reference number: JH0666; MUID:91340162
```

A:Accession: PS0382
A:Molecule type: DNA
A:Residues: 1-15 <LAN>
A:Cross-references: EMBL:X56791
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 51.5%; Score 17; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILERV 7
| | | | |
Db 7 QGVHVT 13

RESULT 7
S09018
hemolytic protein A1 - edible frog (fragment)
C:Species: Rana esculenta (edible frog)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: S09018
R:Simmaco, M.; De Biase, D.; Severini, C.; Alta, M.; Erspamer, G.F.; Barra, D.; Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A:Title: Purification and characterization of bioactive peptides from skin extracts of R.
A:Reference number: S09018; MUID:90198965
A:Accession: S09018
A:Molecule type: protein
A:Residues: 1-13 <SIM>

Query Match 48.5%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7
| | | | |
Db 7 GILSQL 12

RESULT 8
A59018
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C:Accession: A59018
R:Abe, M.; Smith, C.J.; Larson, C.J.
submitted to the Protein Sequence Database, May 1998
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre

A:Reference number: A59018
A:Accession: A59018
A:Molecule type: protein
A:Residues: 1-14 <ABE>
A:Experimental source: Breast cancer cell line MCF-7
A:Note: 3-Val was also found
C:Keywords: DNA binding; heterodimer

Query Match 48.5%; Score 16; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QGILERV 6
| | | | |
Db 9 QIILEK 14

RESULT 9
S19296
16K protein - poulard wheat
C:Species: Triticum turgidum (poulard wheat)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C:Accession: S19296
R:Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.
Biochem. J. 281, 401-405, 1992
A:Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subu
A:Reference number: S19296; MUID:92143804
A:Accession: S19296
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SAN>

Query Match 45.5%; Score 15; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5
| | | | |
Db 7 GLME 10

RESULT 10
I58003
hprt protein - Chinese hamster (fragment)
C:Species: Crictetus griseus (Chinese hamster)
C:Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 14-Nov-1997
C:Accession: I58003
R:Fuscoe, J.C.; Zimmerman, L.J.; Fekete, A.; Setzer, R.W.; Rossiter, B.J.
Mutat. Res. 289, 171-183, 1992
A:Title: Analysis of X-ray-induced HPRT mutations in CHO cells: insertion and deletio
A:Reference number: I58003; MUID:93024555
A:Accession: I58003
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-13 <RES>
A:Cross-references: GB:S46270; NID:g257049
C:Genetics:
A:Gene: hprt

Query Match 45.5%; Score 15; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LERV 7
| | | | |
Db 1 LEKV 4

RESULT 11
S29789
hypothetical protein - Thermoplasma acidophilum (fragment)
C:Species: Thermoplasma acidophilum
C:Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: S29789
R:Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Townner, P.
Eur. J. Biochem. 211, 549-554, 1993
A:Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenas
A:Reference number: S29788; MUID:93170285
A:Accession: S29789
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <BRI>
A:Cross-references: EMBL:X59788

Query Match 45.5%; Score 15; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILERV 7
| | | | |
Db 4 LLKRI 8

RESULT 12

S03530
Ig heavy chain J region (JH-4) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 09-Sep-1997
C:Accession: S03530
R:Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A:Reference number: S01159; MUID:89052653
A:Accession: S03530
A:Molecule type: DNA
A:Residues: 1-14 <SCH>
A:Cross-references: EMBL:X14918; NID:g64805; PID:el6056; PID:g1334657

Query Match 45.5%; Score 15; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QGILERV 7
||| |
DB 6 QGTLVTV 12

RESULT 13

S65392
cytochrome-c oxidase (EC 1.9.3.1) chain VIII-L - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
C:Accession: S65392; S65393; S65391
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A:Reference number: S65372; MUID:95324529
A:Accession: S65392
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SCH>
A:Accession: S65393
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SC2>
A:Accession: S65391
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SC3>
C:Keywords: oxidoreductase

Query Match 45.5%; Score 15; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5
||| |
DB 11 GVLD 14

RESULT 14

PA0075
fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (fra
N:Alternate names: aldolase; fructose-1,6,-bisphosphate triosephosphate-lase
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Nov-1995
C:Accession: PA0075; PA0077
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Reference number: PA0051
A:Accession: PA0075
A:Molecule type: protein
A:Residues: 1-15 <CHO>

A:Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3
A:Accession: PA0077
A:Molecule type: protein
A:Residues: 1-15 <CH2>
A:Note: this form (II) had a molecular weight of 31.6K and an isoelectric point of 5.
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 45.5%; Score 15; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILER 6
| | | |
DB 3 QEVLSR 8

RESULT 15

PA0102
fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (Fusarium sporotrichioides)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Mar-1995
C:Accession: PA0102
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Reference number: PA0051
A:Accession: PA0102
A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 45.5%; Score 15; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILER 6
| | | |
DB 3 QEVLSR 8

RESULT 16

PH1377
T antigen variant K-5 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1377
R:Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992
A:Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for
A:Reference number: PH1373
A:Accession: PH1377
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <DLI>

Query Match 45.5%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
||| |
DB 1 QGI 3

RESULT 17

PT0246
Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0246
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337

A:Accession: PT0246

A:Molecule type: DNA

A:Residues: 1-7 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 42.4%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. NO. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIL 4

DB 5 GIL 7

RESULT 18

S06964

hypothetical protein (nifa 5' region) - Rhizobium leguminosarum (fragment)

C:Species: Rhizobium leguminosarum

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999

C:Accession: S06964

R:Roelink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.

Mol. Microbiol. 3, 1441-1447, 1989

A:Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum PRE-

A:Reference number: S06964; MUID:90136072

A:Accession: S06964

A:Molecule type: DNA

A:Residues: 1-10 <ROE>

A:Cross-references: EMBL:X17073; NID:g46208; PIDN:CAA34923.1; PID:g809748

Query Match 42.4%; Score 14; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. NO. 3.8e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5

DB 5 GVLK 8

RESULT 19

B56899

serum heterodimer, 24K chain - sandbar shark (fragment)

C:Species: Carcharhinus plumbeus (sandbar shark)

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995

C:Accession: B56899

R:Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.

Comp. Biochem. Physiol. B Comp. Biochem. 103, 563-568, 1992

A:Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum by

A:Reference number: A56899; MUID:93092592

A:Accession: B56899

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <VAZ>

C:Keywords: glycoprotein; plasma

Query Match 42.4%; Score 14; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 3.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERV 7

DB 5 ERV 7

RESULT 20

XASNBA

bradykinin-potentiating peptide B - mamushi

C:Species: Aqkistrodon blomhoffi (mamushi)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
C:Accession: A01254

R:Kato, H.; Suzuki, T.

Proc. Jpn. Acad. 46, 176-181, 1970

A:Reference number: A01254

A:Accession: A01254

A:Molecule type: protein

A:Residues: 1-11 <KAT>

A:Note: the sequence of the natural peptide was confirmed by the synthesis and analysis
C:Superfamily: bradykinin-potentiating peptide

C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; v

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 42.4%; Score 14; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. NO. 4.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILER 6

DB 1 QGLPPR 6

RESULT 21

A61483

pyridoxal kinase (EC 2.7.1.35) - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C:Accession: A61483

R:Churchich, J.E.

J. Protein Chem. 9, 613-621, 1990

A:Title: Cleavage of pyridoxal kinase into two structural domains: kinetics of proteo

A:Reference number: A61483; MUID:91197387

A:Accession: A61483

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <CHU>

C:Keywords: homodimer; phosphotransferase

Query Match 42.4%; Score 14; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. NO. 4.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILER 6

DB 8 VLQR 11

RESULT 22

S34065

ornithine decarboxylase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 07-May-1999

C:Accession: S34065

R:Tsirka, S.E.; Turck, C.W.; Coffino, P.

Biochem. J. 293, 289-295, 1993

A:Title: Multiple active conformers of mouse ornithine decarboxylase.

A:Reference number: S34065; MUID:93319524

A:Accession: S34065

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <TSI>

Query Match 42.4%; Score 14; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. NO. 4.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LERV 7

DB 7 LDRI 10

```
RESULT 23
B58503
outer membrane porin protein OprD homolog - unidentified bacterium (fragment)
N:Alternate names: 43K bile stone protein
C:Species: unidentified bacterium
C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58503
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58503
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIN>
A:Experimental source: human bile with stones
A>Note: sequenced along with secondary sequence MXIGVNEXL

Query Match 42.4%; Score 14; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILE 5
Db 7 KGFIE 11

RESULT 24
C33099
148K exoantigen - Plasmodium falciparum (fragment)
C:Species: Plasmodium falciparum
C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 18-Aug-1992
C:Accession: C33099
R:Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A:Reference number: A33098
A:Accession: C33099
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <NIC>

Query Match 42.4%; Score 14; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
Db 3 QGV 5

RESULT 25
PH1467
T-cell receptor beta chain (clone 223/27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1467
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kd
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821
A:Accession: PH1467
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Superfamily: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 42.4%; Score 14; DB 2; Length 12;
```

```
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
Db 7 QGV 9

RESULT 26
H41946
T-cell receptor gamma chain (5t.12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: H41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316
A:Accession: H41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-12 <WHE>
C:Keywords: T-cell receptor

Query Match 42.4%; Score 14; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
Db 5 QGV 7

RESULT 27
JX0315
aminotransferase chimera DX18 - synthetic (fragment)
C:Species: synthetic
C>Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C:Accession: JX0315
R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994
A:Title: Construction of aminotransferase chimeras and analysis of their substrate sp
A:Reference number: JX0315; MUID:94334304
A:Accession: JX0315
A:Molecule type: DNA
A:Residues: 1-12 <MIY>
C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransf
C:Comment: The parental enzymes catalyze the reversible amino group transfer reaction
C:Keywords: aminotransferase

Query Match 42.4%; Score 14; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILER 6
Db 9 LMER 12

RESULT 28
S66235
sperm motility inhibitor protein - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66235
R:Iwamoto, T.; Hiroaki, H.; Furuichi, Y.; Wada, K.; Satoh, M.; Osada, T.;
FEBS Lett. 368, 420-424, 1995
A:Title: Cloning of boar SPMI gene which is expressed specifically in seminal vesicle
A:Reference number: S66233; MUID:95361914
A:Accession: S66235
A>Status: preliminary
```

A;Molecule type: protein
A;Residues: 1-13 <IWA>
A;Note: Pro-6 was also found

Query Match 42.4%; Score 14; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.9e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5
|:|:
Db 10 GVLK 13

RESULT 29

S66234
sperm motility inhibitor protein - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S66234
R;Iwamoto, T.; Hiroaki, H.; Furuichi, Y.; Wada, K.; Satoh, M.; Osada, T.; Gage
FESS Lett. 368, 420-424, 1995
A;Title: Cloning of boar SPMI gene which is expressed specifically in seminal vesicle an
A;Reference number: S66233; MUID:95361914
A;Accession: S66234
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <IWA>
A;Note: Phe-9 and Phe-12 were also found

Query Match 42.4%; Score 14; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5
|:|:
Db 11 GVLK 14

RESULT 30

C44823
synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)
N;Alternate names: superprotein peptide 8
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: C44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:9204785
A;Accession: C44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64253)
C;Keywords: membrane trafficking

Query Match 42.4%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LER 6
|:|:
Db 12 LER 14

Search completed: June 30, 2000, 14:54:17
Job time: 5182 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 19:03:14 ; Search time 39.08 seconds
(without alignments)
5.455 Million cell updates/sec

Title: US-08-833-506c-120

Perfect score: 33

Sequence: 1 QGILERV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 668

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	15	1 ATP2_PINPS	P81663 pinus pinas
2	16	48.5	13	1 HPAL_RANES	P32415 rana escule
3	16	48.5	13	1 NUPM_HUMAN	P51970 homo sapien
4	15	45.5	14	1 YGDH_THEAC	Q05213 thermoplasm
5	15	45.5	15	1 CDN2_LITGI	P56247 litoria gil
6	14	42.4	10	1 TRP5_LEUMA	P81737 leucophaea
7	14	42.4	11	1 BPPB_AGRHA	P01021 agkistrodon
8	14	42.4	12	1 CD11_LITXA	P56245 litoria xan
9	14	42.4	12	1 CD14_LITXA	P56246 litoria xan
10	14	42.4	13	1 CHEP_PARID	P42718 parapolybia
11	14	42.4	13	1 FIBB_HYLLA	P14472 hylobates l
12	14	42.4	13	1 FIBB_MANLE	P14474 mandrillus
13	14	42.4	14	1 MI14_EISFO	P46979 eisenia foe
14	14	42.4	14	1 UN37_CLOPA	P81358 clostridium
15	14	42.4	15	1 LPL_THETH	P21234 thermus aqu
16	14	42.4	15	1 MALT_BACTO	P80072 bacillus th
17	13	39.4	12	1 PA2B_VIPBO	P31859 vipera beru
18	13	39.4	12	1 UP01_CAEEL	P55954 caenorhabdi
19	13	39.4	13	1 CRBL_VESCR	P01518 vespa crabr
20	13	39.4	13	1 FARB_ASCSU	P43173 ascaris suu
21	13	39.4	13	1 HPB9_RANES	P32416 rana escule
22	13	39.4	14	1 CRBL_VESOR	P17236 vespa orien
23	13	39.4	14	1 IF2G_RAT	P81795 rattus norv
24	13	39.4	14	1 MI14_PHEVI	P46980 pheretima v
25	12	36.4	6	1 ACBP_RABIT	P25154 oryctolagus
26	12	36.4	10	1 CU30_LOEMI	P11735 locusta mig
27	12	36.4	10	1 TRP9_LEUMA	P81741 leucophaea
28	12	36.4	10	1 UPAL_HUMAN	P32118 homo sapien
29	12	36.4	11	1 CH60_DROME	P35380 drosophila
30	12	36.4	13	1 CRBL_ICASP	P17237 icaria sp.
31	12	36.4	13	1 CRBL_VESAN	P17233 vespa anali
32	12	36.4	13	1 CRBL_VESLE	P17235 vespa lew
33	12	36.4	13	1 CRBL_VESMA	P17232 vespa manda
34	12	36.4	13	1 CRBL_VESTR	P17231 vespa tropi

35	12	36.4	13	1 CRBL_VESXA	P17234 vespa xanth
36	12	36.4	13	1 UN12_CLOPA	P81353 clostridium
37	12	36.4	13	1 UVRD_SALTY	Q05311 salmonella
38	12	36.4	14	1 ALYT_ALYOB	P08944 alytes obst
39	12	36.4	14	1 SCK3_LEIQU	P45661 leilurus gil
40	12	36.4	15	1 CDN3_LITGI	P56248 litoria gil
41	11	33.3	7	1 UH11_RAT	P56576 rattus norv
42	11	33.3	8	1 ANG2_BOTJA	Q10592 bothrops ja
43	11	33.3	8	1 LCK3_LEUMA	P21142 leucophaea
44	11	33.3	9	1 OXYT_RAJCL	P42994 raja clavav
45	11	33.3	9	1 THYE_PIG	P01255 sus scrofa
46	11	33.3	9	1 ULAE_HUMAN	P31931 homo sapien
47	11	33.3	10	1 ANGL_BOTJA	Q10581 bothrops ja
48	11	33.3	10	1 ANGT_BOVIN	P01017 bos taurus
49	11	33.3	10	1 ANGT_CHICK	P01018 gallus gall
50	11	33.3	10	1 BPP_VIPAS	P31351 vipera aspi
51	11	33.3	10	1 SPI_HAURO	Q10997 halocynthia
52	11	33.3	11	1 BPP4_BOTIN	P30424 bothrops in
53	11	33.3	11	1 BPP_AGRHP	P04562 agkistrodon
54	11	33.3	11	1 CEPI_ACHFU	P22790 achatina fu
55	11	33.3	11	1 HS70_PINPS	P81672 pinus pinas
56	11	33.3	11	1 UN05_CLOPA	P81350 clostridium
57	11	33.3	12	1 TM2A_METMA	P80632 methanosarc
58	11	33.3	13	1 BOML_PSEGU	P42991 pseudophryn
59	11	33.3	13	1 BPP1_BOTJA	P01020 bothrops ja
60	11	33.3	13	1 LPAA_PORGI	P81411 porphyromon
61	11	33.3	13	1 YCIA_SALTY	P25944 salmonella
62	11	33.3	14	1 ANGT_HORSE	P01016 equus cabal
63	11	33.3	14	1 MAST_POLJA	P01517 polistes ja
64	11	33.3	14	1 MAST_VESJA	P01515 vespa xanth
65	11	33.3	15	1 COXI_THUOB	P80978 thunus obe
66	11	33.3	15	1 LMA2_LOEMI	P38497 locusta mig
67	11	33.3	15	1 METK_MAIZE	P80616 zea mays (m
68	11	33.3	15	1 FLAS_MICAE	P10625 microcystis
69	11	33.3	15	1 SCOT_RAT	P01159 rattus norv
70	11	33.3	15	1 UC25_MAIZE	P80631 zea mays (m
71	11	33.3	15	1 URE2_MORMO	P17338 morganella
72	10	30.3	8	1 COXG_RAT	P80430 rattus norv
73	10	30.3	8	1 NS3_MYCTU	P81152 mycobacteri
74	10	30.3	8	1 UH09_RAT	P56575 rattus norv
75	10	30.3	9	1 FIBB_PAPAN	P19344 papio anubi
76	10	30.3	9	1 FIBB_PAPHA	P19343 papio hamad
77	10	30.3	9	1 FIBB_THEGE	P19342 theropitheci
78	10	30.3	9	1 TAL1_PICJA	P17440 pichia jadi
79	10	30.3	9	1 TAL3_PICJA	P17441 pichia jadi
80	10	30.3	9	1 ULAK_MOUSE	P99031 mus musculu
81	10	30.3	10	1 TKN1_SCYCA	P81863 pardachirus
82	10	30.3	10	1 TKNB_CHICK	P08608 scyllorhinu
83	10	30.3	10	1 TKNB_CONMY	P19851 gallus gall
84	10	30.3	10	1 TKNB_RANCA	P28500 oncorhynch
85	10	30.3	10	1 TKNB_RANCI	P22689 rana catesb
86	10	30.3	10	1 TKNB_RANCI	P22689 rana catesb
87	10	30.3	10	1 TKNK_PIG	P01292 sus scrofa
88	10	30.3	10	1 TKNK_PIG	P01292 sus scrofa
89	10	30.3	10	1 TKN_PHYBI	P08610 phyllomedus
90	10	30.3	10	1 TKS1_AEDAE	P42634 aedes aegyp
91	10	30.3	10	1 TKS2_AEDAE	P42635 aedes aegyp
92	10	30.3	10	1 UP11_CAEEL	P55956 caenorhabdi
93	10	30.3	10	1 XYNB_DICB4	P80717 dictyoglomu
94	10	30.3	11	1 ANGT_CRIGE	P09037 crinia geor
95	10	30.3	11	1 PVK_PERAM	P41837 periplaneta
96	10	30.3	11	1 TKN1_PSEGU	P42986 pseudophryn
97	10	30.3	11	1 TKN2_UPERU	P08612 uperoleia r
98	10	30.3	11	1 TKN2_PSEGU	P42987 pseudophryn
99	10	30.3	11	1 TKN2_UPERU	P08616 uperoleia r
100	10	30.3	11	1 TKN3_PSEGU	P42988 pseudophryn

ALIGNMENTS

RESULT_1
ATP2_PINPS

ID ATP2_PINPS STANDARD; PRT; 15 AA.
AC P81663;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
GN ATPB.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RX MEDLINE; 93274088.
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
CC SUBUNIT (BY SIMILARITY).
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N153) IS: 5.5, ITS MW IS: 55 KD.
CC -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC PROSITE: PS00152; ATPASE_ALPHA_BETA; PARTIAL.
DR ATP synthesis; CF(1); Hydrogen ion transport;
KW Hydrolase; ATP-binding; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1629 MW; 3580CB725CCB8D9 CRC64;

Query Match 60.6%; Score 20; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILE 5
||:|
DB 7 QGVLD 11

RESULT 2
HPAL_RANES STANDARD; PRT; 13 AA.
ID HPAL_RANES
AC P32415;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE HEMOLYTIC PROTEIN A1 (FRAGMENT).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Raninae; Rana.
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RX MEDLINE; 90198965.
RA Simmaco M., de Blase D., Severini C., Alta M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: SKIN.
DR PIR: S09018; S09018.
KW Amphibian skin; Amidation; Hemolysis.

FT MOD_RES 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

Query Match 48.5%; Score 16; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 GILERV 7
||:|
DB 7 GILSQL 12

RESULT 3
NUPM_HUMAN
ID NUPM_HUMAN STANDARD; PRT; 13 AA.
AC P51970;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (EC 1.6.5.3)
DE (EC 1.6.99.3) (COMPLEX I-19KD) (COMPLEX I-PGIV) (CI-PGIV)
DE (FRAGMENT).
GN NDUF8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE.
RC TISSUE=KIDNEY;
RX MEDLINE; 97295305.
RA Sarto C., Marocchi A., Sanchez J.-C., Giannone B., Frutiger S.,
RA Golaz O., Wilkins M.R., Doro G., Cappellano F., Hughes G.J.,
RA Hochstrasser D.F., Mocarelli P.;
RT "Renal cell carcinoma and normal kidney protein expression.";
RL Electrophoresis 18:599-604(1997).
CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC TO BE UBIQUINONE.
CC -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
CC THIS IS A COMPONENT OF THE HYDROPHOBIC FRACTION.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 19 KD SUBUNIT FAMILY.
DR SWISS-2DPAGE; P51970; HUMAN.
DR MIM: 603359; .
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1428 MW; 5A64EE91C92AF767 CRC64;

Query Match 48.5%; Score 16; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GILE 5
||:|
DB 2 GIVE 5

RESULT 4
YGDH_THEAC STANDARD; PRT; 14 AA.
ID YGDH_THEAC
AC Q05213;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL PROTEIN IN GLUCOSE DEHYDROGENASE GENE 3'REGION
DE (FRAGMENT).
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
OC Thermoplasma.

RNA SEQUENCE FROM N.A.
RC STRAIN-DSM 1728:
RX MEDLINE; 93170285.
RT "Cloning, sequencing and expression of the gene encoding glucose
RT dehydrogenase from the thermophilic archaeon Thermoplasma
RT acidophilum";
RL Eur. J. Biochem. 211:549-554(1993).
CC -----
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CC -----
DR EMBL; X59788; CAA42451.1; -.
DR PIR; S29789; S29789.
KW Hypothetical protein.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1674 MW; 685A1FFF36529944 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILERV 7
Db 4 LLKRI 8

RESULT 5
CDN2_LITGI STANDARD; PRT; 15 AA.
AC P56247;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CAERIDIN 2.
OS Litoria gilleni.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hyllidae; Litoria.
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-PAROTOID GLAND;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni";
RL J. Chem. Res. 139:937-961(1993).
CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN PAROTOID AND/OR ROSTRAL
CC GLANDS.
CC -1- MASS SPECTROMETRY: MW-1408; METHOD-FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 15
SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF272550CBF CRC64;

Query Match 45.5%; Score 15; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7
Db 1 GLLDVV 6

RESULT 6
TRP5_LEUMA

ID TRP5_LEUMA STANDARD; PRT; 10 AA.
AC P81737;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TACHYKININ-RELATED PEPTIDE 5 (LEMRP 5).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
[1]
RN SEQUENCE.
RP TISSUE-MIDGUT;
RC MEDLINE; 97053012.
RX Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms";
RL Regul. Pept. 65:185-196(1996).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-BRAIN;
RX MEDLINE; 97269266.
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT Madeira cockroach; evidence for tissue-specific expression of
RT isoforms";
RL Peptides 18:7-15(1997).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT AND BRAIN.
CC -1- MASS SPECTROMETRY: MW-1033.2; METHOD-WALDI-MS.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1033 MW; C452CD66D9C8769D CRC64;

Query Match 42.4%; Score 14; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
Db 7 QGV 9

RESULT 7
BPPB_AKGHA STANDARD; PRT; 11 AA.
ID BPPB_AKGHA
AC P01021;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE B (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Agkistrodon halys blomhoffii (Mamushi) (Gloydius blomhoffii).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
OC Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae;
OC Agkistrodon.
RN [1]
RP SEQUENCE.
RC TISSUE-VENOM;
RA Kato H., Suzuki T.;
RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
RT the venom of Agkistrodon halys blomhoffii";
RL Proc. Jpn. Acad. B, Phys. Biol. Sci. 46:176-181(1970).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; A01254; XASNEA.
KW Hypotensive agent; Venom.

FT MOD_RES 1 1 PYREOLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGILER 6
Db 1 QGLPPR 6

RESULT 8
CD11_LITXA
ID CD11_LITXA STANDARD; PRT; 12 AA.
AC P56245; P81253;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CAERIDIN 1.1/1.2/1.3.
OS Litoria xanthomera (Orange-thighed frog), Litoria splendida,
Litoria gilleni, and Litoria chloris (Blue-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES=L.XANTHOMERA;
RX MEDLINE; 97374000.
RA Steinborner S.T.; Waugh R.J.; Bowie J.H., Wallace J.C., Tyler M.J.,
Ramsay S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
Australian tree frog Litoria xanthomera.";
RL J. Pept. Sci. 3:181-185(1997).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES=L.SPLENIDA; TISSUE=PAROTOID GLAND;
RX Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
caeridin 1 from Litoria splendida.";
RL J. Chem. Soc. Perkin Trans. 1:3173-3178(1992).
RN [3]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES=L.GILLEN; TISSUE=PAROTOID GLAND;
RX Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.,
Hu P., Gross M.L.;
RT "Two isomeric alpha and beta aspartyl dodecapeptides and their
cyclic amino succinyl analogue from the Australian tree frog
Litoria gilleni.";
RL Aust. J. Chem. 48:1981-1987(1995).
RN [5]
RP SEQUENCE.
RC SPECIES=L.CHLORIS; TISSUE=SKIN;
RX MEDLINE; 98175802.
RA Steinborner S.T.; Currie G.J.; Bowie J.H., Wallace J.C., Tyler M.J.;
RT "New antibiotic caerin 1 peptides from the skin secretion of the
Australian tree frog Litoria chloris. Comparison of the activities of
the caerin 1 peptides from the genus Litoria.";
RL J. Pept. Res. 51:121-126(1998).
RN [1]
RP FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS IN L.
XANTHOMERA OR SPECIFICALLY BY THE SKIN PAROTOID AND/OR ROSTRAL
GLANDS IN L. SPLENIDA AND L. GILLEN.
CC -1- PTM: ISOMERIZATION ALPHA-BETA OF THE ASP-4 RESIDUE IN CAERIDIN
1.2; A CYCLIC SUCCINIMIDE MAY BE FORMED BETWEEN ASP-4 AND GLY-5

CC RESIDUES IN CAERIDIN 1.3.
CC -1- MASS SPECTROMETRY: MM-1140; METHOD=FAB.
CC -1- MISCELLANEOUS: THE RESULTS FOR MASS SPECTROMETRY OF CAERIDIN 1.1
IS 1140 IN REF.1, REF.3 AND REF.4, WHILE IN REF.2 IT IS 1139.
CC Amphibian skin; Amidation.
KW MOD_RES 12 12 AMIDATION
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILE 5
Db 1 GLLD 4

RESULT 9
CD14_LITXA
ID CD14_LITXA STANDARD; PRT; 12 AA.
AC P56246;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CAERIDIN 1.4.
OS Litoria xanthomera (Orange-thighed frog), and
Litoria chloris (Blue-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Litoria.
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC SPECIES=L.XANTHOMERA;
RX MEDLINE; 97374000.
RA Steinborner S.T.; Waugh R.J.; Bowie J.H., Wallace J.C., Tyler M.J.,
Ramsay S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
Australian tree frog Litoria xanthomera.";
RL J. Pept. Sci. 3:181-185(1997).
RN [2]
RP SEQUENCE.
RC SPECIES=L.CHLORIS; TISSUE=SKIN;
RX MEDLINE; 98175802.
RA Steinborner S.T.; Currie G.J.; Bowie J.H., Wallace J.C., Tyler M.J.;
RT "New antibiotic caerin 1 peptides from the skin secretion of the
Australian tree frog Litoria chloris. Comparison of the activities of
the caerin 1 peptides from the genus Litoria.";
RL J. Pept. Res. 51:121-126(1998).
RN [1]
RP FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM-1096; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 12 12 AMIDATION
SQ SEQUENCE 12 AA; 1097 MW; 28225503E3772728 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILE 5
Db 1 GLLD 4

RESULT 10
CHEP_PARID
ID CHEP_PARID STANDARD; PRT; 13 AA.
AC P42718;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

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DE CHEMOTACTIC PEPTIDE.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Polistinae; Parapolybia.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RT Parapolybia indica.";
RL Eisei Dobutsu 39:105-111(1988).
KW Chemotaxis; Amidation.
FT MOD_RES 13 13
SQ SEQUENCE 13 AA; 1298 MW; 5C950CE8E39D5873 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 2.4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7
DB 3 GLLKGI 8

RESULT 11
FIBB_HYLLA STANDARD; PRT; 13 AA.
ID FIBB_HYLLA
AC P14472;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIBRINOPEPTIDE B.
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
RN [1]
RP SEQUENCE.
RX MEDLINE; 70294424.
RA Moss G.A., Doolittle R.F., Roberts B.F.;
RT "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT at position B-3.";
RL Science 170:468-470(1970).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
DR Blood coagulation; Plasma.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 11 13
FT VARIANT 11 13 S -> G.
SQ SEQUENCE 13 AA; 1406 MW; 7D944D60187D698F CRC64;

Query Match 42.4%; Score 14; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
DB 1 QGV 3

RESULT 12
FIBB_MANLE STANDARD; PRT; 14 AA.
ID FIBB_MANLE
AC P14474;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIBRINOPEPTIDE B.
OS Mandrillus leucophaeus (Drill) (Papio leucophaeus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
OC Mandrillus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 691115139.
RA Doolittle R.F., Glasgow C., Moss G.A.;
RT "Characterization of fibrinopeptides A and B from a drill (Mandrillus
RT leucophaeus).";
RL Biochim. Biophys. Acta 175:217-219(1969).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
DR Blood coagulation; Plasma.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 14 14
FT VARIANT 14 14
SQ SEQUENCE 14 AA; 1434 MW; 6695B0F11EF72E1B CRC64;

Query Match 42.4%; Score 14; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
DB 1 QGV 3

RESULT 13
MY14_EISFO STANDARD; PRT; 14 AA.
ID MY14_EISFO
AC P46979;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MYOACTIVE TETRADECAPEPTIDE (ETP).
OS Eلسenia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eلسenia.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=GUT;
RX MEDLINE; 96087879.
RA Ukema K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eلسenia
RT foetida.";
RL Peptides 16:995-999(1995).
CC -1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC MUSCLES.
CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD_RES 14 14
FT VARIANT 14 14
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match 42.4%; Score 14; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 2.6e+03;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 2 GILERV 7
| :| :
Db 5 GAADRI 10

RESULT 14
UN37_CLOPA
ID UN37_CLOPA STANDARD; PRT; 14 AA.
AC P81358;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN CP 37 FROM 2D-PAGE (FRAGMENT).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
RP SEQUENCE.
RC STRAIN-W5;
RX MEDLINE; 98291870.
RA Flengstad R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
NON_TER 14 14
FT PROTEIN IS: 5.8, ITS MW IS: 44.7 KD.
SQ SEQUENCE 14 AA; 1579 MW; 05384662DEF89210 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 14;
Best Local Similarity 56.7%; Pred. No. 2.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OG1 3
| :| :
Db 10 QGV 12

RESULT 15
LPL_TETH
ID LPL_TETH STANDARD; PRT; 15 AA.
AC P21234;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE LEU LEADER PEPTIDE.
OS Thermus aquaticus (subsp. thermophilus).
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HB8;
RX MEDLINE; 88121725.
RA Croft J.E., Love D.R., Bergquist P.L.;
RT "Expression of leucine genes from an extremely thermophilic bacterium
in Escherichia coli.";
RL Mol. Gen. Genet. 210:490-497(1987).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF LEUCINE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X06604; CAA29823.1; -
DR PIR; S00901; LFTWL.
KW Leader peptide; Leucine biosynthesis.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Query Match 42.4%; Score 14; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILER 6
| :| :|
Db 8 VLDR 11

RESULT 16
MALT_BACTO
ID MALT_BACTO STANDARD; PRT; 15 AA.
AC P80072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE MALTASE (EC 3.2.1.20) (ALPHA-GLUCOSIDASE I) (FRAGMENT).
OS Bacillus thermoamyloliquefaciens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE.
RC STRAIN-KP1071 / FERM P8477;
RX MEDLINE; 92209510.
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
RT "Assignment of Bacillus thermoamyloliquefaciens KP1071
alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
and in structural parameters calculated from the amino acid
composition.";
RL Eur. J. Biochem. 205:249-256(1992).
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING
1,4-LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC PIR; S21240; S21240.
DR Hydrolase; Glycosidase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;

Query Match 42.4%; Score 14; DB 1; Length 15;
Best Local Similarity 14.3%; Pred. No. 2.7e+03;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 OGILERV 7
| :| :| :
Db 8 EGVYQI 14

RESULT 17
PA2B_VIPBO
ID PA2B_VIPBO STANDARD; PRT; 12 AA.
AC P31859;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PHOSPHOLIPASE A2, BASIC (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE
2-ACYLHYDROLASE) (FRAGMENT).
OS Vipera berus orientalis (Viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
OC Squamata; Scieroglossa; Serpentes; Colubroidea; Viperidae; Viperinae;
OC Vipera.
RN [1]
RP SEQUENCE.
RC TISSUP-VENOM;
RX MEDLINE; 74128698.
RA Delori P.J.;
RT "Purification and physicochemical, chemical and biological properties
of a toxic A2 phospholipase isolated from the venom of viperidae
snakes; Vipera berus.";
RL Biochimie 55:1031-1045(1973).

CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES.
 CC CATALYTIC ACTIVITY: PHOSPHATIDYLCHOLINE + H(2)O -> 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 KW Hydrolyase; Lipid degradation; Calcium; Venom.
 FT NON_TER 12
 FT SEQUENCE 12 AA; 1412 MW; D054351A89969879 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILE 5
 Db 9 ILE 11

RESULT 18
 UP01_CABEL
 ID UP01_CABEL STANDARD; PRT; 12 AA.
 AC P55954;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 1) (FRAGMENT).
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 CC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=BRISTOL N2;
 RA MEDLINE; 97295299.
 RX Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
 RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
 RT homogenates and identification of protein spots by microsequencing.";
 RL Electrophoresis 18:557-562(1997).
 FT NON_TER 12
 FT SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match 39.4%; Score 13; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ILE 6
 Db 6 IMEX 9

RESULT 19
 CBRL_VESCR
 ID CBRL_VESCR STANDARD; PRT; 13 AA.
 AC P01518;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CRABROLIN.
 OS Vespa crabro (European hornet).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Vespidae; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RX MEDLINE; 84289390.
 RA Argiolas A., Pisano J.J.;
 RT "Isolation and characterization of two new peptides, mastoparan C and
 RT crabrolin, from the venom of the European hornet, Vespa crabro.";
 RL J. Biol. Chem. 259:10106-10111(1984).

RN [2]
 RN SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
 RX MEDLINE; 97419326.
 RA Krishnakumari V., Nagaraj R.;
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue
 RT peptide from the venom of the European hornet, Vespa crabro, and its
 RT analogs.";
 RL J. Pept. Res. 50:88-93(1997).
 CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
 CC OF NEUTROPHILS. HAS ANTIMICROBIAL AND HEMOLYTIC ACTIVITY.
 DR PIR; A01781; JZVHP1.
 KW Mast cell degranulation; Chemotaxis; Venom; Amidation; Antibiotic.
 FT MOD_RES 13
 FT SEQUENCE 13 AA; 1497 MW; 515EF9FCFA8D2407 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ILE 7
 Db 5 ILRKI 9

RESULT 20
 FARB_ASCSU
 ID FARB_ASCSU STANDARD; PRT; 13 AA.
 AC P43173;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFAMIDE-LIKE NEUROPEPTIDE AFIL.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 CC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Ascaridida;
 CC Ascaridoidea; Ascarididae; Ascaris.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 95380362.
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
 RT Ascaris suum.";
 RL Peptides 16:491-500(1995).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 13
 FT SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILE 5
 Db 4 GISE 7

RESULT 21
 HPB9_RANES
 ID HPB9_RANES STANDARD; PRT; 13 AA.
 AC P32416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HEMOLYTIC PROTEIN B9 (FRAGMENT).
 OS Rana esculenta (Edible frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 CC Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Raninae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;

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RX MEDLINE: 90198965.
RA Simmaco M., de Blase D., Severini C., Alta M., Erspaner G.F.,
RA Baria D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Blochm. Biophys. Acta 1033:318-323(1990).
CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: SKIN.
DR PIR: S09019; S09019.
KW Amphibian skin; Amidation; Hemolysis.
FT MOD_RES 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1402 MW: C6B41A765DF9287D CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;
Best Local Similarity 33.3%; Pred. No. 4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7
DB 7 GLLGKL 12

RESULT 22
CRBL_VESOR STANDARD; PRT; 14 AA.
AC P17236;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last annotation update)
DE HISTAMINE RELEASING PEPTIDE II (HR-II).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespidae; Vespinae; Vespinae; Vespa.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Miroshnikov A. I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
CC OF NEUTROPHILS.
DR PIR: JN0390; JN0390.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 14 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1524 MW: 22015B4A6CEDFD38 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 OGIL 4
DB 11 KGLL 14

RESULT 23
IF2G_RAT STANDARD; PRT; 14 AA.
AC P81795;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE EUKARYOTIC TRANSLATION INITIATION FACTOR 2 GAMMA SUBUNIT (EIF-2-
DE GAMMA) (PP42) (FRAGMENT).
GN EIF2S3 OR EIF2G.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RA MEDLINE: 96374441.
RA Gil C., Plana M., Riera M., Itarte E.;
RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eif-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA. THIS
CC COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING
CC TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL
CC SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY
CC HYDROLYSIS OF THE GTP BOUND TO EIF-2 AND RELEASE OF AN EIF-2-GDP
CC BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER
CC ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP
CC BY WAY OF A REACTION CATALYZED BY EIF-2B.
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN.
CC -1- SIMILARITY: TO GTP-DEPENDENT ELONGATION FACTORS.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1511 MW: D86EDA955ABEFA12 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILER 6
DB 10 GIVSK 14

RESULT 24
MY14_PHEVI STANDARD; PRT; 14 AA.
AC P46980;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MYOACTIVE TETRADECAPEPTIDE (PTP).
OS Pheretima vittata (Earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbriclna; Megascolecidae; Pheretima.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=GUT;
RA MEDLINE: 96087879.
RA Ukena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT foetida.";
RL Peptides 16:995-999(1995).
CC -1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC MUSCLES.
CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD_RES 14 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1522 MW: DA40BEE67CCD91AD CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 4.3e+03;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7
DB 5 GSADRI 10

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RESULT 25
ACPH_RABIT
ID ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ACYLAMINO-ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
DE (APH) (ACYLAMINOACYL-PEPTIDASE) (FRAGMENT).
GN APEH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RC TISSUE=MUSCLE;
RX MEDLINE; 92222120.
RX Krishna R.G., Chin C.C.Q., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
CC ACID + PEPTIDE.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE
CC PROLYL OLIGOPEPTIDASE FAMILY.
DR PROSITE; PS00708; PRO-ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 8.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LER 6
DB 1 MER 3

RESULT 26
CU30_LOCFI
ID CU30_LOCFI STANDARD; PRT; 10 AA.
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CUTICLE PROTEIN 30 (LM-30) (LM-ACP 30) (FRAGMENT).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
RN [1]
RP SEQUENCE.
RX MEDLINE; 86108304.
RX Hoejrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of
RT cuticular proteins from the migratory locust, Locusta migratoria.";
RL Eur. J. Biochem. 154:153-159(1986).
CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF MIGRATORY LOCUST WHICH
CC CONTAINS MORE THAN 100 DIFFERENT STRUCTURAL PROTEINS.
DR PIR; C24802; C24802.
KW Structural protein; Cuticle.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 969 MW; 4973E36B58772877 CRC64;
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Query Match 36.4%; Score 12; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIL 4
DB 1 GLL 3

RESULT 27
TRP9_LEUMA
ID TRP9_LEUMA STANDARD; PRT; 10 AA.
AC P81741;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TACHYKININ-RELATED PEPTIDE 9 (LEMPRP 9).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=BRAIN;
RX MEDLINE; 97269266.
RX Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT madeira cockroach; evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- MASS SPECTROMETRY: MW=1081.5; METHOD=MALDI-MS.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1081 MW; 9E469D6D9C87685 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
DB 7 QGM 9

RESULT 28
URAL_HUMAN
ID URAL_HUMAN STANDARD; PRT; 10 AA.
AC P32118;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF RED BLOOD CELLS (SPOT 1) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RC TISSUE=ERYTHROCYTE;
RX MEDLINE; 94147970.
RX Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RX Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RX Balant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 23 KD.
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DR SWISS-2DPAGE; P32118; HUMAN.
FT NON_TER 1
NON_TER 10
SQ SEQUENCE 10 AA; 977 MW; 723C65BIADD0587B CRC64;

Query Match 36.4%; Score 12; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 OGI 3
Db 3 EGI 5

RESULT 29
CH60_DROME
ID CH60_DROME STANDARD; PRT; 11 AA.
AC P33380;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MITOCHONDRIAL MATRIX PROTEIN P1 (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
GN MMP-P1 OR HSP60.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE.
RC STRAIN=VALLECAS; TISSUE=WING IMAGINAL DISK;
RX MEDLINE; 93272852.
RA Santaren J.F., van Damme J., Puype M., Vandekerckhove J., Garcia-Bellido A.
RT "Identification of Drosophila wing imaginal disc proteins by two-dimensional gel analysis and microsequencing."
RL Exp. Cell Res. 206:220-226(1993).
CC -!- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR FLYBASE: FBgn0010375; Mmp-P1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; PARTIAL.
KW Chaperone; ATP-binding; Mitochondrion.
FT NON_TER 1
NON_TER 11
SQ SEQUENCE 11 AA; 1243 MW; 78501A366365A6DB CRC64;

Query Match 36.4%; Score 12; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 ILER 6
Db 2 IIEQ 5

RESULT 30
CRBL_ICASP
ID CRBL_ICASP STANDARD; PRT; 13 AA.
AC P17237;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CHEMOTACTIC PEPTIDE (I-CP).
OS Icaria sp. (Ropalididae wasp).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vespoidea; Vespidae; Polistinae; Icaria.
RN [1]
RP SEQUENCE.
RC TISSUE=VENOM;
RA Yasuhara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
RL (In) Izumiya N. (eds.);
RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation, Osaka (1985).
RL -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.
KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
FT MOD_RES 13
MOD_RES 13 AMIDATION.
SQ SEQUENCE 13 AA; 1353 MW; 348DBC7AA30A3768 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 GIL 4
Db 10 GLL 12

Search completed: June 30, 2000, 19:03:16
Job time: 15039 sec

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Run on: June 30, 2000, 16:18:45 ; Search time 53.11 Seconds
(without alignments)
9.138 Million cell updates/sec

Title: US-08-833-506c-120
Perfect score: 33
Sequence: 1 QGILERV 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

SPTREMBL_12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	57.6	11	2	Q44237
2	19	57.6	15	2	Q54325
3	17.5	53.0	14	12	O10234
4	17	51.5	13	2	P74844
5	17	51.5	13	4	Q16406
6	16	48.5	11	7	O77910
7	16	48.5	12	2	Q53183
8	16	48.5	13	4	Q16007
9	16	48.5	15	12	Q97090
10	15	45.5	10	2	Q9X3M2
11	15	45.5	10	13	O73594
12	15	45.5	11	2	Q9X9S6
13	15	45.5	11	7	O77911
14	15	45.5	13	2	Q9X3J6
15	15	45.5	13	2	Q9X3E1
16	15	45.5	13	3	P87031
17	15	45.5	15	10	O65177
18	15	45.5	15	12	Q97092
19	15	45.5	15	12	Q97094
20	14.5	43.9	14	12	O10226

21	14.5	43.9	14	12	O10227	O10227 human immun
22	14.5	43.9	14	12	O10228	O10228 human immun
23	14.5	43.9	14	12	O10229	O10229 human immun
24	14.5	43.9	14	12	O10230	O10230 human immun
25	14.5	43.9	14	12	O10232	O10232 human immun
26	14.5	43.9	14	12	O10233	O10233 human immun
27	14.5	43.9	14	12	O10235	O10235 human immun
28	14	42.4	8	6	Q28866	Q28866 megaptera n
29	14	42.4	9	4	O15892	O15892 homo sapien
30	14	42.4	9	4	P78484	P78484 homo sapien
31	14	42.4	10	2	Q60192	Q60192 spiroplasma
32	14	42.4	10	2	Q60194	Q60194 spiroplasma
33	14	42.4	10	2	Q52837	Q52837 rhizobium l
34	14	42.4	10	12	O64971	O64971 alfalfa mos
35	14	42.4	12	2	Q46039	Q46039 citrobacter
36	14	42.4	12	2	Q53358	Q53358 escherichia
37	14	42.4	13	2	Q55094	Q55094 synechocyst
38	14	42.4	14	2	Q54861	Q54861 streptococc
39	14	42.4	14	4	Q14342	Q14342 homo sapien
40	14	42.4	15	2	Q46013	Q46013 caulobacter
41	14	42.4	15	8	O78794	O78794 pylaella l
42	14	42.4	15	12	Q79359	Q79359 human immun
43	14	42.4	15	12	Q97098	Q97098 human immun
44	13	39.4	8	2	Q9X3K1	Q9X3K1 prochloroco
45	13	39.4	9	6	O46574	O46574 ovis aries
46	13	39.4	10	12	Q88082	Q88082 chimpanzee
47	13	39.4	10	12	Q82625	Q82625 infectious
48	13	39.4	11	4	Q15997	Q15997 homo sapien
49	13	39.4	12	2	P97134	P97134 rhizobium l
50	13	39.4	12	12	O10421	O10421 influenza a
51	13	39.4	13	2	Q47601	Q47601 escherichia
52	13	39.4	13	2	Q9XBV0	Q9XBV0 nitrogen-fi
53	13	39.4	13	11	Q54684	Q54684 cricetus
54	13	39.4	14	2	Q47599	Q47599 escherichia
55	13	39.4	14	6	Q9XSL4	Q9XSL4 capra hircu
56	13	39.4	14	8	P92076	P92076 euhadra her
57	13	39.4	14	12	O10231	O10231 human immun
58	13	39.4	15	2	O69173	O69173 yersinia pe
59	13	39.4	15	2	O52640	O52640 pseudomonas
60	12	36.4	7	12	Q66113	Q66113 cherry leaf
61	12	36.4	8	2	Q51594	Q51594 escherichia
62	12	36.4	8	11	O64024	O64024 mus musculu
63	12	36.4	8	11	O64025	O64025 mus spretus
64	12	36.4	9	4	O95574	O95574 homo sapien
65	12	36.4	9	12	Q84333	Q84333 simian viru
66	12	36.4	10	5	Q25355	Q25355 locusta mig
67	12	36.4	10	5	Q25356	Q25356 locusta mig
68	12	36.4	11	7	O77871	O77871 oreochromis
69	12	36.4	11	7	O77872	O77872 oreochromis
70	12	36.4	11	7	O77873	O77873 oreochromis
71	12	36.4	11	12	Q83083	Q83083 leucania se
72	12	36.4	12	6	O46664	O46664 macropus ro
73	12	36.4	13	4	Q14804	Q14804 homo sapien
74	12	36.4	14	2	Q47335	Q47335 escherichia
75	12	36.4	14	2	Q92B42	Q92B42 streptococc
76	12	36.4	14	2	Q9X715	Q9X715 campylobact
77	12	36.4	14	2	Q9WW79	Q9WW79 campylobact
78	12	36.4	14	5	Q26075	Q26075 psammochinu
79	12	36.4	14	10	Q9XGM4	Q9XGM4 arabidopsis
80	12	36.4	15	2	O52059	O52059 salmonella
81	12	36.4	15	5	O97430	O97430 drosophila
82	12	36.4	15	8	Q35921	Q35921 salmo salar
83	12	36.4	15	12	Q85713	Q85713 rous sarcom
84	11	33.3	8	2	Q45889	Q45889 clostridium
85	11	33.3	8	7	Q16468	Q16468 homo sapien
86	11	33.3	8	7	Q29810	Q29810 homo sapien
87	11	33.3	8	10	Q42507	Q42507 triticum ae
88	11	33.3	8	11	Q63898	Q63898 rattus norv
89	11	33.3	8	12	Q83977	Q83977 influenza a
90	11	33.3	9	12	O71069	O71069 canine herpes
91	11	33.3	9	12	O66545	O66545 human herpes
92	11	33.3	9	12	O83622	O83622 murray vall
93	11	33.3	9	12	Q85723	Q85723 simian sarc

94 11 33.3 10 8 Q35013 meloidogyne
 95 11 33.3 10 8 Q9XMB4 aegilops sq
 96 11 33.3 11 2 Q47604 escherichia
 97 11 33.3 11 2 P71228 escherichia
 98 11 33.3 11 4 Q16217 homo sapien
 99 11 33.3 11 4 O94785 homo sapien
 100 11 33.3 11 11 Q62207 mus musculu

ALIGNMENTS

RESULT 1
 Q44237
 ID Q44237 PRELIMINARY; PRT; 11 AA.
 AC Q44237;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 02, Last annotation update)
 DE GLUTAMINE SYNTHETASE (FRAGMENT).
 GN GLNA.
 OS Anabaena sp.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PC6 7120;
 RA WARNER L.E., LIGON P.J., STAHEL A.W., CURTIS S.E.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PC6 7120;
 RA SCAPPINO L.A.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U21853; AAA65652.1; -.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1316 MW; 0427DF84 CRC32;

Query Match 57.6%; Score 19; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 4.6e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QGILERV 7
 Db 5 QEVLRKI 11

RESULT 2
 Q54325
 ID Q54325 PRELIMINARY; PRT; 15 AA.
 AC Q54325;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE CHLORAMPHENICOL ACETYLTRANSFERASE (FRAGMENT).
 GN CAT.
 OS Staphylococcus intermedius.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PCW6;
 RA LODDER G., SCHWARZ S., GREGORY P., DYKE K.;
 RL "Tandem duplication in ermC translational attenuator of the macrolide-
 RT lincosamide-streptogramin B resistance plasmid pSES6 from
 RT Staphylococcus equorum.";
 RL Antimicrob. Agents Chemother. 40:215-217(1996).
 DR EMBL; X82666; CAA57981.1; -.
 FT Transferase.
 NON_TER 1
 SQ SEQUENCE 15 AA; 1931 MW; 996BDE4C CRC32;

Query Match 57.6%; Score 19; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 QGILERV 7
 Db 5 QDIHRV 11

RESULT 3
 O10234
 ID O10234 PRELIMINARY; PRT; 14 AA.
 AC O10234;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98216723.
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
 RA BENEDETTO A.;
 RT "Grossly defective nef gene sequences in a human immunodeficiency
 RT virus type 1-seropositive long-term nonprogressor.";
 RL J. Virol. 72:3646-3657(1998).
 DR EMBL; U89854; AAC26093.1; -.
 DR PFAM; PF00517; GP41; 1.
 KW Envelope protein.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1733 MW; CBF88541 CRC32;

Query Match 53.0%; Score 17.5; DB 12; Length 14;
 Best Local Similarity 71.4%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 QGILERV 7
 Db 7 QG-LERI 12

RESULT 4
 P74844
 ID P74844 PRELIMINARY; PRT; 13 AA.
 AC P74844;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE SIGMA FACTOR (FRAGMENT).
 GN FLIA.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168-94;
 RX MEDLINE; 97311993.
 RA BURNENS A.P., STANLEY J., SACK R., HUNZIKER P., BRODARD I.,
 RA NICOLET J.;
 RT "The flagellin N-methylase gene fljB and an adjacent serovar-specific
 RT IS200 element in Salmonella typhimurium.";
 RL Microbiology 143:1539-1547(1997).
 DR EMBL; Z67749; CAA91563.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1459 MW; 0D3A47E3 CRC32;

Query Match 51.5%; Score 17; DB 2; Length 13;
 Best Local Similarity 16.7%; Pred. No. 1.6e+03;

Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILER 6

Db :|:|:|:| 13

RESULT 5

Q16406 ID Q16406 PRELIMINARY; PRT; 13 AA.

AC Q16406;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)

DE GHRH-R PROTEIN (FRAGMENT).

GN GHRH-R.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 96001284.

RA HASHIMOTO K., KOGA M., MOTOMURA T., KASAYAMA S., KOUHARA H.,

RA OHNISHI T., ARIITA N., HAYAKAWA T., SATO B., KISHIMOTO T.;

RT "Identification of alternatively spliced messenger ribonucleic acid

RT encoding truncated growth hormone-releasing hormone receptor in human

RT pituitary adenomas";

RL J. Clin. Endocrinol. Metab. 80:2933-2939(1995).

DR EMBL; S79912; AAD14318.1; -.

FT NON_TER 1

SQ SEQUENCE 13 AA; 1612 MW; 085914B2 CRC32;

Query Match

Best Local Similarity 51.58; Score 17; DB 4; Length 13;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7

Db :|:|:| 13

RESULT 6

Q77910 ID Q77910 PRELIMINARY; PRT; 11 AA.

AC Q77910;

DT 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DE MHC CLASS II B LOCUS 3 (FRAGMENT).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;

OC Perciformes; Labroidae; Cichlidae; Oreochromis.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 98315113.

RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,

RA SUELTMANN H., FIGUEROA F., KLEIN J.;

RT "Linkage relationships and haplotype polymorphism among cichlid Mhc

RT class II B loci";

RL Genetics 149:1527-1547(1998).

DR EMBL; AF050021; AAC41360.1; -.

FT NON_TER 1

FT NON_TER 11

SQ SEQUENCE 11 AA; 1344 MW; 2E9158C4 CRC32;

Query Match

Best Local Similarity 48.58; Score 16; DB 7; Length 11;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7

Db :|:|:| 6

Db 1 GFLEYI 6

RESULT 7

Q53183 ID Q53183 PRELIMINARY; PRT; 12 AA.

AC Q53183;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE BETA-SUBUNIT OF NITRILE HYDRATASE (FRAGMENT).

OS Rhodococcus sp.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=N-774;

RX MEDLINE; 95072315.

RA HASHIMOTO Y., NISHIYAMA M., HORINOCHI S., BEPPU T.;

RT "Nitrile hydratase gene from Rhodococcus sp. N-774 requirement for its

RT downstream region for efficient expression";

RL Biosci. Biotechnol. Biochem. 58:1859-1865(1994).

DR EMBL; D30033; BAA06273.1; -.

DR HSSP; P13449; IAHJ.

FT NON_TER 1

SQ SEQUENCE 12 AA; 1323 MW; 666FD346 CRC32;

Query Match

Best Local Similarity 48.58; Score 16; DB 2; Length 12;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OGILE 5

Db :|:|:| 9

RESULT 8

Q16007 ID Q16007 PRELIMINARY; PRT; 13 AA.

AC Q16007;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE LYSOSOMAL ACID BETA-GALACTOSIDASE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 91369478.

RA MORREAU H., BONTEIN E., ZHOU X.Y., D'AZZO A.;

RT "Organization of the gene encoding human lysosomal beta-

RT galactosidase";

RL DNA Cell Biol. 10:495-504(1991).

DR EMBL; S59584; AAB19814.1; -.

FT NON_TER 13

SQ SEQUENCE 13 AA; 1482 MW; 615C03BB CRC32;

Query Match

Best Local Similarity 48.58; Score 16; DB 4; Length 13;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GILERV 7

Db :|:|:| 8

Db 3 GFLVRI 8

RESULT 9

Q97090

ID Q97090 PRELIMINARY; PRT; 15 AA.
 AC Q97090;
 DT 01-FEB-1997 (TReMBLrel. 02, Created)
 DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE GAG POLYPROTEIN (FRAGMENT).
 GN GAG.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LAI;
 RX MEDLINE; 96184535.
 RA WEI Q., FULTZ P.N.;
 RT "Extensive diversification of human immunodeficiency virus type 1
 RT subtype B strains during dual infection of a chimpanzee that
 RT progressed to AIDS.";
 RL J. Virol. 72:3005-3017(1998).
 DR EMBL; U56889; AAC59299.1; -.
 KW Polyprotein.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1577 MW; 6B94DD64 CRC32;

Query Match 48.5%; Score 16; DB 12; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 OGIL 6
 Db 10 EGDLD 15

RESULT 10
 Q9X3M2 PRELIMINARY; PRT; 10 AA.
 ID Q9X3M2;
 AC Q9X3M2;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 [1]
 RP SEQUENCE FROM N.A.
 RA URBACH E., CHISHOLM S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream.";
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL; AF070219; AAD23269.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1076 MW; BCB27A24 CRC32;

Query Match 45.5%; Score 15; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OGIL 3
 Db 5 OGIL 7

RESULT 11
 Q73594 PRELIMINARY; PRT; 10 AA.
 ID Q73594;
 AC Q73594;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE ZAX-2 (FRAGMENT).

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WHITE LEHORN; TISSUE=WHOLE EMBRYOS;
 RX MEDLINE; 98141813.
 RA PEALE F.V., MASON K., HUNTER A.W., BOTHWELL M.;
 RT "Multiplex display polymerase chain reaction amplifies and resolves
 RT related sequences sharing a single moderately conserved domain.";
 RL Anal. Biochem. 256:158-168(1998).
 DR EMBL; U34617; AAC36455.1; -.
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1068 MW; 381E8670 CRC32;

Query Match 45.5%; Score 15; DB 13; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERV 7
 Db 5 GLPKRV 10

RESULT 12
 Q9X9S6 PRELIMINARY; PRT; 11 AA.
 ID Q9X9S6;
 AC Q9X9S6;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).
 GN ORE9.
 OS Streptomyces lividans.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TK21;
 RX MEDLINE; 99328982.
 RA MARTINEZ-COSTA O.H., MARTIN-TRIANA A.J., MARTINEZ E.,
 RA FERNANDEZ-MORENO M.A., MALPARTIDA F.;
 RT "An additional regulatory gene for actinorhodin production in
 RT Streptomyces lividans involves a LysR-type transcriptional
 RT regulator.";
 RL J. Bacteriol. 181:4353-4364(1999).
 DR EMBL; Y18818; CAB51138.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1160 MW; C64AD8BF CRC32;

Query Match 45.5%; Score 15; DB 2; Length 11;
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 OGILERV 7
 Db 2 QGVRAHV 8

RESULT 13
 O77911 PRELIMINARY; PRT; 11 AA.
 ID O77911;
 AC O77911;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE MHC CLASS II B LOCUS 3 (FRAGMENT).
 OS Oryzochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 RN Perciformes; Labroidae; Cichlidae; Oreochromis.
 RX SEQUENCE FROM N.A.
 RX MEDLINE; 98315113.
 RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,
 RA SUELTSMANN H., FIGUEROA F., KLEIN J.,
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc
 RT class II B loci."
 RL Genetics 149:1527-1547(1998).
 DR EMBL; AF050022; AAC41361.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1401 MW; FF3CDDF9 CRC32;

Query Match 45.5%; Score 15; DB 7; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILE 5
 Db 1 GFLE 4

RESULT 14
 O9X3J6 PRELIMINARY; PRT; 13 AA.
 AC O9X3J6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA URBACH E., CHISHOLM S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL; AF070189; AAD23225.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1473 MW; ECD3C1B2 CRC32;

Query Match 45.5%; Score 15; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
 Db 7 QGI 9

RESULT 15
 ID O9X3E1 PRELIMINARY; PRT; 13 AA.
 AC O9X3E1;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE CYTOCHROME B (FRAGMENT).
 GN PETB.
 OS Prochlorococcus sp.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA URBACH E., CHISHOLM S.W.;

RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream."
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL; AF070141; AAD20755.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1434 MW; 14865A9B CRC32;

Query Match 45.5%; Score 15; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
 Db 7 QGI 9

RESULT 16
 P87031 PRELIMINARY; PRT; 13 AA.
 AC P87031;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE ORF YGR126W (FRAGMENT).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA VAN DYCK L., SKALA J., DE WERGIFOSSE P., PURNELLE B., TALLA E.,
 RA NAWROCKI A., DEL BINO S., GOFFEAU A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 272912; CAA97139.2; -.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1594 MW; AC1F58C5 CRC32;

Query Match 45.5%; Score 15; DB 3; Length 13;
 Best Local Similarity 28.6%; Pred. No. 4.4e+03;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QGILERV 7
 Db 5 KGFFHRI 11

RESULT 17
 O65177 PRELIMINARY; PRT; 15 AA.
 AC O65177;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE TURGOR RESPONSIVE PROTEIN HOMOLOG (FRAGMENT).
 OS Mesembryanthemum crystallinum (Common ice plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Caryophyllales; Alzooceae;
 OC Mesembryanthemum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ROOT;
 RA MICHALOWSKI C.B., BOHNERT H.J.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF054444; AAC14178.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1607 MW; AD52368C CRC32;

Db 7 QG-LER 11

RESULT 22

O10228 PRELIMINARY; PRT; 14 AA.
AC O10228;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL; U89848; AAC26087.1; -.
DR PFAM; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

RESULT 23

O10229 PRELIMINARY; PRT; 14 AA.
AC O10229;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL; U89849; AAC26088.1; -.
DR PFAM; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

RESULT 24

O10230 PRELIMINARY; PRT; 14 AA.
AC O10230;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL; U89850; AAC26089.1; -.
DR PFAM; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

RESULT 25

O10232 PRELIMINARY; PRT; 14 AA.
AC O10232;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL; U89852; AAC26091.1; -.
DR PFAM; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6

Db 7 QG-LER 11

RESULT 26

O10233

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ID O10233 PRELIMINARY; PRT; 14 AA.
AC O10233;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DE 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DE 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
RT virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL: U89853; AAC26092.1; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6
Db 7 QG-LER 11

RESULT 27
O10235 PRELIMINARY; PRT; 14 AA.
ID O10235;
AC O10235;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
RA BENEDETTO A.;
RT "Grossly defective nef gene sequences in a human immunodeficiency
RT virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL: U89855; AAC26094.1; -.
DR PFAM: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match 43.9%; Score 14.5; DB 12; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QGILER 6
Db 7 QG-LER 11

RESULT 28
Q28866 PRELIMINARY; PRT; 8 AA.
ID Q28866;
AC Q28866;
DT 01-NOV-1996 (TRENBLrel. 01, Created)

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DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE ACTIN PROTEIN (FRAGMENT).
GN ACTIN.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Cetacea; Mysticeti; Balaeopteridae;
OC Megaptera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94285813.
RA PALUMBI S.R., BAKER C.S.;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435(1994).
DR EMBL: S73467; AAD14118.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 906 MW; 4D7C9EF6 CRC32;

Query Match 42.4%; Score 14; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
Db 6 QGV 8

RESULT 29
Q15892 PRELIMINARY; PRT; 9 AA.
ID Q15892;
AC Q15892;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-AUG-1998 (TRENBLrel. 07, Last annotation update)
DE (CLONE XP3B4) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PLACENTA;
RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XIONG M.,
RA COOLBAUGH M.I., CHINAULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,
RA CASKEY C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL: L32071; AAA73882.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 971 MW; A5838DF1 CRC32;

Query Match 42.4%; Score 14; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LER 6
Db 2 LER 4

RESULT 30
P78484 PRELIMINARY; PRT; 9 AA.
ID P78484;
AC P78484;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE FYN ONCOGENE, 3' END, CLONE PFYN-C-11. (FRAGMENT).
GN FYN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE OF 90-98 FROM N.A.
RX MEDLINE; 88234523.
RA KAWAKAMI T., KAWAKAMI Y., AARONSON S.A., ROBBINS K.C.;
RT "Acquisition of transforming properties by FYN, a normal SRC-related
human gene."
RL Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874(1988).
DR EMBL; M20284; AAN52491.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1143 MW; C710793C CRC32;

Query Match 42.4%; Score 14; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGILE 5
| |
Db 4 QSFLE 8

Search completed: June 30, 2000, 16:18:47
Job time: 7898 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 13:12:33 ; Search time 40.56 Seconds
(without alignments)
4.088 Million cell updates/sec

Title: US-08-833-506c-89
Perfect score: 35
Sequence: 1 VTQDDLQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 76368

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	9	1 W81229	Human INOS peptide
2	35	100.0	9	1 W81294	Human INOS peptide
3	35	100.0	9	1 W81264	Human INOS peptide
4	35	100.0	12	1 W81228	Human INOS peptide
5	35	100.0	12	1 W81293	Human INOS peptide
6	35	100.0	12	1 W81268	Human INOS peptide
7	35	100.0	15	1 W81227	Human INOS peptide
8	35	100.0	15	1 W81292	Human INOS peptide
9	35	100.0	15	1 W81267	Human INOS peptide
10	31	88.6	15	1 W81223	Human INOS peptide
11	31	88.6	15	1 W81288	Human INOS peptide
12	30	85.7	10	1 W81265	Human INOS peptide
13	30	85.7	10	1 W81270	Human INOS peptide
14	26	74.3	9	1 W81266	Human INOS peptide
15	23	65.7	15	1 R20282	Beta-2 integrin pe
16	23	65.7	15	1 W02070	Human beta2 integr
17	22	62.9	8	1 W53913	Interleukin-1 rece
18	22	62.9	12	1 W35486	Proteoglycan-assoc
19	22	62.9	13	1 W35498	Pal A peptide from
20	22	62.9	14	1 W12358	Human hsp60 peptid
21	22	62.9	14	1 R33050	Human heat shock p
22	21	60.0	6	1 R29290	Nerve growth stimu
23	21	60.0	6	1 W05563	Ependymin peptide
24	21	60.0	9	1 W97963	Human synaptosomal
25	21	60.0	10	1 W97904	Human synaptosomal
26	21	60.0	11	1 R25221	Residues 150-160 o
27	21	60.0	14	1 R86681	Allergen Alt a 45
28	21	60.0	14	1 W30922	Birch pollen aller
29	20	57.1	6	1 W81217	Human INOS peptide
30	20	57.1	6	1 W81230	Human INOS peptide
31	20	57.1	6	1 W81295	Human INOS peptide
32	20	57.1	6	1 W81283	Human INOS peptide
33	20	57.1	6	1 W81269	Human INOS peptide
34	20	57.1	9	1 W81216	Human INOS peptide

ALIGNMENTS

RESULT 1
W81229

ID W81229 standard; peptide; 9 AA.
AC W81229;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5267.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9 /note= "Gln residue amidated"
FT W09845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.
DT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 36; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 9 AA;
SQ Sequence

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9
RESULT 2
ID W81294
AC W81294 standard; peptide; 9 AA.
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment for epitope mapping #15.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9 /note= "Gln residue amidated"
FT W09845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.
DT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Fig 7b; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and

CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 9 AA;
SQ Sequence

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9
RESULT 3
ID W81264
AC W81264 standard; peptide; 9 AA.
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5215.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 9 /note= "Gln residue amidated"
FT W09845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.
DT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 12; Page 53; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention. 9 AA;
SQ Sequence

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9
RESULT 4
ID W81228
AC W81228 standard; peptide; 12 AA.
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5266.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VTQDDLQ 7
DB 3 VTQDDLQ 9
RESULT 4
ID W81228
AC W81228 standard; peptide; 12 AA.
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5266.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW

KW monoclonal antibody; mimic: quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified_site 12 /note= "Asn residue amidated"
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Page 36; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 12 AA;
 SQ Sequence 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDDLQ 7
 Db 3 VTQDDDLQ 9

RESULT 5

W81293
 ID W81293 standard; peptide; 12 AA.
 AC W81293;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment for epitope mapping #14.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7B; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the

CC invention.
 SQ Sequence 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDDLQ 7
 Db 3 VTQDDDLQ 9

RESULT 6

W81268
 ID W81268 standard; peptide; 12 AA.
 AC W81268;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5266.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified_site 15 /note= "Lys residue amidated"
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 12; Page 54; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 12 AA;

QY 1 VTQDDDLQ 7
 Db 3 VTQDDDLQ 9

Query Match 100.0%; Score 35; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDDLQ 7
 Db 3 VTQDDDLQ 9

RESULT 7

W81227
 ID W81227 standard; peptide; 15 AA.
 AC W81227;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5265.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers

PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Page 35; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 15 AA;
 SQ Sequence 15 AA;

Query Match 88.6%; Score 31; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
 Db 1 TQDDLQ 6
 |||||

RESULT 11
 W81288

ID W81288 standard; peptide; 15 AA.
 AC W81288;
 DE 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment for epitope mapping #9.
 DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7A; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 15 AA;
 SQ Sequence 15 AA;

Query Match 88.6%; Score 31; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.89;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
 |||||

Db 1 TQDDLQ 6
 |||||

RESULT 12
 W81265
 ID W81265 standard; peptide; 9 AA.
 AC W81265;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5236.
 DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified_site 9
 FT W09845710-A1.
 PN 15-OCT-1998.
 PD 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunoassay in which a sample is contacted with a specific binding
 PT entity reactive with human iNOS or mimics.
 PS Example 12; Page 53; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g. a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention. 9 AA;
 SQ Sequence 9 AA;

Query Match 85.7%; Score 30; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6
 |||||

Db 4 VTQDDL 9
 |||||

RESULT 13
 W81270
 ID W81270 standard; peptide; 10 AA.
 AC W81270;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5269.
 DE Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified_site 10
 FT W09845710-A1.
 PN 15-OCT-1998.
 PD 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an

PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 12; Page 54; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 10 AA;

Query Match 85.7%; Score 30; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6
| | | | |
DB 5 VTQDDL 10

RESULT 14
W81266
ID W81266 standard; peptide; 9 AA.
AC W81266;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5257.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers

FT Modified_site 9 /note= "Asp residue amidated"
FT W09845710-A1.

PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-66777.
PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI; 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.

PS Example 12; Page 53; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 9 AA;

Query Match 74.3%; Score 26; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5
| | | | |
DB 5 VTQDD 9

RESULT 15
R20282
ID R20282 standard; peptide; 15 AA.
AC R20282;
DT 10-APR-1992 (first entry)
DE Beta-2 integrin peptide derived from CD11b alpha subunit.
KW Immune response; phagocyte-mediated tissue damage; A domain; MAM;
KW inflammation; CD11/CD18 complex; alpha subunit; CR3; M01; Mav-1;
KW complement receptor type 3; heterodimer; collagen binding.
OS Synthetic.
PN W09119511-A.
PD 26-DEC-1991.
PF 18-JUN-1991; U04338.
PR 18-JUN-1990; US-539842.
PR 04-JAN-1991; US-637830.
PA (GEHO-) GEN HOSPITAL CORP.
PI Arnaout MA;
DR WPI; 92-024197/03.
PT Beta-2 integrin peptide CD11b, recombinant hetero-dimer
PT CD11b/CD18 - or MAB against them; useful for inhibiting CD11/CD18
PT mediated immune response in control of phagocyte-mediated tissue
PT damage
PS Claim 8; Page 73; 84pp; English.
CC The peptide (SEQ ID NO: 29) corresponds to residues 750-764 of CD11b
CC alpha subunit of beta 2 integrin. The peptide may be synthesised or
CC prep'd. by recombinant techniques using the gene, the sequence of
CC which was disclosed by Arnaout et al., J. Cell Biol. 106:2153 (1988).
CC (References are also provided for the DNA sequences of human CD18,
CC CD11c and CD11a). The peptide is capable of inhibiting a CD11/CD18
CC mediated immune response and is useful for treatment of ischaemia
CC reperfusion injury, burns, frostbite, acute arthritis, asthma and
CC adult respiratory distress syndrome. It may also be used to block
CC intra-islet infiltration of macrophages associated with insulin-
CC dependent diabetes mellitus, and for controlling phagocyte-media-
CC ted tissue damage to heart muscle during acute cardiac insuffi-
CC ciency.
CC See also R20256-R20299.
SQ Sequence 15 AA;

Query Match 65.7%; Score 23; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 43;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDL 6
| | | | |
DB 10 ICQDDL 15

RESULT 16
W02070
ID W02070 standard; peptide; 15 AA.
AC W02070;
DT 09-APR-1997 (first entry)
DE Human beta2 integrin subunit CD11b, residues 750-764.
KW Beta2 integrin; A-domain; metal binding domain; inflammatory response;
KW immune response; inhibition; phagocyte-mediated tissue injury;
KW inflammation.
OS Homo sapiens.
PN W09624063-A1.
PD 08-AUG-1996.
PF 30-JAN-1996; U01314.
PR 30-JAN-1995; US-380167.
PA (GEHO) GEN HOSPITAL CORP.
PI Arnaout MA;
DR WPI; 96-371576/37.

PT In vitro identification of integrin function antagonists - by
PT measuring binding of A-domain peptide derived from integrin to
PT ligand in presence and absence of candidate antagonist
PS Disclosure; Page 11; 111pp; English.
CC The sequences given in W02037-80 represent peptides derived from
CC beta2 integrin, esp. A-domain and the metal binding domains. These

CC peptides were selected using the method of the invention which
 CC screens compounds for their ability to inhibit the binding of a
 CC selected integrin to a ligand which naturally binds to it. The
 CC method comprises measuring the binding of an A-domain peptide
 CC derived from the selected integrin, to the ligand in the presence
 CC and absence of the test compound and determining whether the binding
 CC is decreased. Identified compounds are capable of interfering with
 CC certain cellular immune/inflammatory responses, particularly
 CC phagocyte-mediated tissue injury and inflammation. The numbering
 CC of the amino acid residues is based on the the deduced amino acid
 CC sequence of the open reading frame of human CD11b from Arnaout et al.,
 CC J. Cell. Biol. 106:2153 (1988).
 CC Sequence 15 AA;
 SQ

Query Match 65.7%; Score 23; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 43;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDL 6
 Db 10 ICQDDL 15
 : ||||

RESULT 17

W53913
 ID W53913 standard; Peptide; 8 AA.

DE 17-AUG-1998 (first entry)
 DE Interleukin-1 receptor accessory molecule K320-K327.
 DE Interleukin-1 receptor accessory molecule; IL-1R ACN; human;
 KW signal transduction; agonist; antagonist; antibody; infection;
 KW septic shock; inflammation; rheumatoid arthritis; therapy; epitope;
 KW antigen.

OS Homo sapiens.
 PN W09808969-A1.
 PD 05-MAR-1998.
 PF 26-AUG-1996; U13954.
 PR 26-AUG-1996; W0-U13954.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Bednarik DP, Olsen HS, Rosen CA;
 DR WPI; 98-230267/20.

PT Nucleic acid encoding interleukin-1 receptor accessory protein -
 PT used for therapeutic modulation of IL-1 activity
 PS Claim 17; Page 83; 95pp; English.
 CC This peptide corresponds to amino acids 320-327 of novel human
 CC interleukin-1 receptor accessory molecule (IL1-R ACN) (see W53897),
 CC a new member of the immunoglobulin superfamily that forms a complex
 CC with type 1 IL1-R. It comprises an epitope-bearing portion of
 CC IL1-R ACN. 18 Antigenic peptides comprising epitope-bearing
 CC portions of human IL1-R ACN are claimed (see W53898-915). These
 CC can be used to generate soluble IL1-R ACN-specific antibodies,
 CC and may be produced by chemical synthesis or by recombinant means
 CC using nucleic acid molecules (see V23659) of the invention. The
 CC antibodies are useful as immunoassay reagents for detecting
 CC IL1-R ACN, for affinity purification of IL1-R ACN and for
 CC identifying cells that express IL1-R ACN.
 CC Sequence 8 AA;
 SQ

Query Match 62.9%; Score 22; DB 1; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.5e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
 Db 2 VTSEDLK 8
 : |||

RESULT 18

W35486

ID W35486 standard; peptide; 12 AA.
 AC W35486;

DT 22-APR-1998 (first entry)
 DE Proteoglycan-associated lipoprotein peptide 1.
 KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 OS scaffold; inhibition; metastasis; wound healing; solid phase.
 PN Actinobacillus pleuropneumoniae.
 PD W09738011-A1.
 PF 16-OCT-1997.
 PR 03-APR-1997; D00146.
 PR 03-APR-1996; DK-000398.
 PA (PEPR-) PEPRESEARCH AS.
 PI Heegaard PMH, Jakobsen PH;
 DR WPI; 97-512645/47.
 PT Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives
 PS Example 5; Page 89; 262pp; English.
 CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence
 CC represents a peptide used in an example from the present invention. An
 CC (A)-solid phase complex can be used as a scaffold for the production of
 CC chemical derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an immunostimulating complex (iscom) resulting an
 CC (A)-iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease.
 CC Sequence 12 AA;
 SQ

Query Match 62.9%; Score 22; DB 1; Length 12;
 Best Local Similarity 57.1%; Pred. No. 54;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
 Db 2 MTAEDLQ 8
 : || |||

RESULT 19

W35498

ID W35498 standard; peptide; 13 AA.

AC W35498;
 DT 22-APR-1998 (first entry)
 DE Pal A peptide from W09738011.
 KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis; wound healing; solid phase.
 OS Unidentified.
 PN W09738011-A1.
 PD 16-OCT-1997.
 PR 03-APR-1997; D00146.
 PR 03-APR-1996; DK-000398.
 PA (PEPR-) PEPRESEARCH AS.
 PI Heegaard PMH, Jakobsen PH;
 DR WPI; 97-512645/47.
 PT Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives
 PS Example 7; Page 99; 262pp; English.

CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and

CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence
 CC represents a peptide used in an example from the present invention. An
 CC (A)-solid phase complex can be used as a scaffold for the production of
 CC chemical derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold-peptide for
 CC the incorporation into an Immunostimulating Complex (Iscom) resulting in
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-, laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic-(A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease.
 SQ Sequence 13 AA;

Query Match 62.9%; Score 22; DB 1; Length 13;
 Best Local Similarity 57.1%; Pred. No. 59;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDQL 7
 :|:|:
 Db 3 MTAEQL 9

RESULT 20

ID W12358 standard; protein; 14 AA.
 AC W12358;
 DT 13-NOV-1997 (first entry)
 DE Human hsp60 peptide p39 (343-366).
 KW Heat-shock protein; hsp; hsp60; insulin-dependent diabetes mellitus;
 KW IDDM.
 OS Homo sapiens.
 PN W09701959-A1.
 PD 23-JAN-1997.
 PF 01-JUL-1996; U11375.
 PR 30-JUN-1995; IL-114407.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Abulafia R, Bockova J, Cohen IR, Elias D;
 DR WPI: 97-108693/10.
 DT New peptide(s) derived from human heat-shock protein 60 - used for
 PT early diagnosis, prevention and treatment of insulin-dependent
 PT diabetes mellitus
 PS Claim 1: Page 13; 49pp; English.
 CC The peptides given in W12346 to W12358 are derived from human hsp60
 CC (W12345) and are useful for early diagnosis of IDDM by detecting,
 CC in the blood or urine, antibodies or T-cells immunologically
 CC reactive with human hsp60 (presence of which indicates high
 CC probability of diabetes or its subsequent development).
 CC Other peptides (W12359 to W12361) were shown not to be as
 CC effective.
 SQ Sequence 14 AA;

Query Match 62.9%; Score 22; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5
 :|:|:
 Db 8 VTKDD 12

RESULT 21

ID W33050 standard; peptide; 14 AA.
 AC W33050;
 DT 26-JAN-1998 (first entry)

DE Human heat shock protein 60 residues 343-366.
 KW Treatment; T cell mediated; disease; condition; antigen; human;
 KW inflammatory T cell; pathogenesis; heat shock protein 60; hsp60;
 KW insulin dependent diabetes mellitus; IDDM.
 OS Homo sapiens.
 PN W09702016-A1.
 PD 23-JAN-1997.
 PF 02-JUL-1996; U11373.
 PR 03-JUL-1995; IL-114458.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Cohen IR, Elias D, Shinitzky M;
 DR WPI: 97-108732/10.
 DT Prepn. for treatment of T cell mediated diseases such as diabetes or
 PT multiple sclerosis - comprises antigen recognised by inflammatory T
 PT cells, and a fat emulsion carrier comprising e.g. soybean oil, egg
 PT phospholipid and glycerol
 PS Disclosure; Page 6; 39pp; English.
 CC A preparation for the treatment of T cell mediated diseases or
 CC conditions, comprises a carrier, comprising 10-20% triglycerides
 CC and 1.2-2.4% phospholipids of plant and/or animal origin,
 CC 2.25-4.5% osmo-regulator, 0-0.05% antioxidant and sterile water
 CC (to 100 ml), and an antigen recognised by inflammatory T cells
 CC associated with the pathogenesis of the disease or condition. The
 CC preparation can be used to treat insulin dependent diabetes
 CC mellitus, when the antigen is a peptide derived from heat shock
 CC protein 60 (e.g. the present peptide). The emulsions promote a TH1
 CC to TH2 cytokine shift.
 SQ Sequence 14 AA;

Query Match 62.9%; Score 22; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 65;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5
 :|:|:
 Db 8 VTKDD 12

RESULT 22

R29290
 ID R29290 standard; peptide; 6 AA.
 AC R29290;
 DT 07-APR-1993 (first entry)
 DE Nerve growth stimulating protein fragment.
 KW Ependymin; neuroactive domain; treatment; Huntington's chorea;
 KW Parkinson's disease; Alzheimer's disease.
 OS Synthetic.
 PN W09220362-A.
 PD 26-NOV-1992.
 PF 14-MAY-1991; U03346.
 PR 14-MAY-1991; WO-U03346.
 PA (SHAS/) SHASHOUA VE.
 PI Shashoua VE.
 DR WPI: 92-415465/50.
 PT Protein fragment comprising neuro-active domain of ependymin -
 PT enhances nerve connectivity and growth and is for treating
 PT nervous system disorders e.g. Huntington's, Parkinson's and
 PT Alzheimer's diseases
 PS Claim 21: Page 53; 77pp; English.
 CC The fragment is that of an active region of the ependymin neuroactive
 CC domain (gamma chain amino acids 164-169) effective in stimulating nerve
 CC growth and elongation. It is 85.7% homologous to epidermal growth
 CC factor amino acids 169-175. It can be used to treat nerve injuries
 CC and to correct genetic or systemic disorders, e.g. treatment of
 CC Huntington's, Parkinson's or Alzheimer's diseases, or to pretreat
 CC nerve tissue before transplantation. It can be administered in
 CC sustained release form and may be coupled to a carrier which protects
 CC it against decomposition in the stomach and blood stream after oral
 CC admin. and carries it across the blood brain barrier, opt. with
 CC subsequent release of the free fragment in the brain.
 SQ Sequence 6 AA;

Query Match 60.0%; Score 21; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
 ||||
 Db 1 DDLQ 4

RESULT 23
 W05563
 ID W05563 standard; peptide; 6 AA.
 AC W05563;
 DT 09-DEC-1996 (first entry)
 DE Ependymin peptide fragment #8.
 KW Ependymin; nerve growth factor; glycoprotein; extracellular fluid; brain;
 KW cerebrospinal fluid; therapy; stroke recovery; neurodegenerative disease;
 KW neuron transplantation; memory loss; brain-penetration.
 OS Synthetic.
 PN US5545719-A.
 PD 13-AUG-1996.
 PF 01-MAY-1990; 517159.
 PR 01-MAY-1990; US-517159.
 PR 14-MAY-1991; US-700653.
 PR 24-FEB-1994; US-201046.
 PA (NEUR-) NEUROMEDICA INC.
 PI Shashoua VE;
 DR WPI; 96-383719/38.
 PT New ependymin peptide fragments - useful for promoting nerve growth
 PS Claim 1; Column 23; 19pp; English.
 CC W05566-W05583 represent fragments of the nerve growth factor ependymin.
 CC Ependymin is a glycoprotein dimer. The protein is synthesised by
 CC specific cells which secrete and maintain a steady state concentration of
 CC the protein in the extracellular and cerebrospinal fluids of the brain.
 CC Ependymin is a nerve growth promoter, but it is not currently known how
 CC it functions. These sequences promote nerve growth, and may be used as
 CC therapy to enhance recovery after stroke, to counteract age-related
 CC memory loss, or to treat neurodegenerative diseases. These sequences can
 CC also be used for research purposes, such as in neuron transplantation
 CC studies. Fatty acid conjugates of these peptides (using 16-22c fatty
 CC acids) have an increased brain-penetration index, and may be used for the
 CC same purposes.
 CC Sequence 6 AA;
 SQ

Query Match 60.0%; Score 21; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
 ||||
 Db 1 DDLQ 4

RESULT 24
 W97963
 ID W97963 standard; Peptide; 9 AA.
 AC W97963;
 DT 21-JUN-1999 (first entry)
 DE Human synaptonemal complex protein 1 (SCP-1) HLA binding motif.
 KW SCP-1; synaptonemal complex protein 1; human; spermatocyte;
 KW meiosis; tumour; marker; breast cancer; ovary cancer; glioma;
 KW renal cell carcinoma; transformed cell; diagnosis; therapy;
 KW vaccine; antibody; HLA; major histocompatibility complex; MHC.
 OS Homo sapiens.
 PN W09904040-A1.
 PD 28-JAN-1999.
 PF 25-JUN-1998; U13209.
 PR 15-JUL-1997; US-892702.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Pfreundschuh M, Sahin U, Tureci O;
 DR WPI; 99-132280/11.

PT Detecting transformed cells from expression of synaptonemal complex
 PT protein - for diagnosis, prevention and treatment of cancer
 PS Example 6; Page 12; 37pp; English.
 CC This peptide corresponds to amino acids 42-50 the previously
 CC known human synaptonemal complex protein 1 (SCP-1), a protein
 CC that is involved in meiosis and which is expressed in tumour cells,
 CC especially in renal cell carcinomas, gliomas and breast carcinomas,
 CC but not in healthy cells except for testis. The peptide is
 CC presumed to bind to MHC molecule B44. It is one of 83 peptides (see
 CC W97901-83) derived from SCP-1 and identified as HLA binding motifs.
 CC Complexes formed between a peptide and an HLA molecule should
 CC provoke a cytolytic T cell response. The invention provides
 CC immunotherapeutic approaches to conditions characterised by
 CC aberrant or abnormal levels of one or more SCP proteins.
 SQ Sequence 9 AA;

Query Match 60.0%; Score 21; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.5e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
 ||||
 Db 1 TEDDFE 6

RESULT 25
 W97904
 ID W97904 standard; Peptide; 10 AA.
 AC W97904;
 DT 21-JUN-1999 (first entry)
 DE Human synaptonemal complex protein 1 (SCP-1) HLA binding motif.
 KW SCP-1; synaptonemal complex protein 1; human; spermatocyte;
 KW meiosis; tumour; marker; breast cancer; ovary cancer; glioma;
 KW renal cell carcinoma; transformed cell; diagnosis; therapy;
 KW vaccine; antibody; HLA; major histocompatibility complex; MHC.
 OS Homo sapiens.
 PN W09904040-A1.
 PD 28-JAN-1999.
 PF 25-JUN-1998; U13209.
 PR 15-JUL-1997; US-892702.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PI Pfreundschuh M, Sahin U, Tureci O;
 DR WPI; 99-132280/11.

PT Detecting transformed cells from expression of synaptonemal complex
 PT protein - for diagnosis, prevention and treatment of cancer
 PS Example 6; Page 10; 37pp; English.
 CC This peptide corresponds to amino acids 41-50 of the previously
 CC known human synaptonemal complex protein 1 (SCP-1), a protein
 CC that is involved in meiosis and which is expressed in tumour cells,
 CC especially in renal cell carcinomas, gliomas and breast carcinomas,
 CC but not in healthy cells except for testis. The peptide is
 CC presumed to bind to MHC molecule A1. It is one of 83 peptides (see
 CC W97901-83) derived from SCP-1 and identified as HLA binding motifs.
 CC Complexes formed between a peptide and an HLA molecule should
 CC provoke a cytolytic T cell response. The invention provides
 CC immunotherapeutic approaches to conditions characterised by
 CC aberrant or abnormal levels of one or more SCP proteins.
 SQ Sequence 10 AA;

Query Match 60.0%; Score 21; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 71;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
 ||||
 Db 2 TEDDFE 7

RESULT 26
 R25221
 ID R25221 standard; Protein; 11 AA.


```

AC R25221:
DE 23-DEC-1992 (first entry)
KW Residues 150-160 of mature apoE.
KW Inhibit lymphocyte proliferation; ovarian androgen secretion;
KW ovaries; low density lipoprotein receptor; LDL; steroidogenesis;
KW hepatic LDL-binding; autoimmune diseases; arthritis;
KW polycystic ovaries; hypercholesterolaemia.
OS Synthetic.
PN W09210512-A.
PD 25-JUN-1992.
PF 10-DEC-1991; U09269.
PR 10-DEC-1990; US-625093.
PR 30-SEP-1991; US-769629.
PR 09-DEC-1991; US-805193.
PA (SCRI) SCRIPPS RES INST.
PI Curtiss LK, Dyer CA, Smith R;
DR WPI; 92-234586/28.
PT Immunosuppressive polypeptide analogues of apolipoprotein E - for
PT modulating lymphocyte proliferation and ovarian androgen
PT synthesis, e.g. for treating inflammation, polycystic ovaries,
PT hypercholesterolaemia, and in diagnosis
PS Example 1; Page 59; 118pp; English.
CC This sequence was synthesised together with R25220-6 and a
CC lymphocyte cell culture system to examine the ability of various
CC polypeptides and conjugates to mimic the ability of apoE to inhibit
CC lymphocyte differentiation as evidence by proliferation. It was
CC found that they had no effect on lymphocyte proliferation when
CC used in nonconjugated monomeric form. However, when these
CC peptides were used conjugated to bovine serum albumin (BSA)
CC lymphocyte proliferation was inhibited in an equivalent manner by
CC all peptides studied as evidenced by decreasing amounts of
CC thymide uptake with increasing dose of conjugate. See also R25211-26.
SQ Sequence 11 AA;

Query Match 60.0%; Score 21; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
DB 4 DDLQ 7

RESULT 27
R8681
ID R8681 standard; Peptide; 14 AA.
AC R8681;
DE 19-AUG-1996 (first entry)
DE Allergen Alt a 45 T-cell epitope 1.
KW Alt a 45; Alt a 12; allergen; epitope; immunoglobulin E; IgE;
KW detection; immunotolerance; anergy.
OS Alternaria alternata.
PN AT9402038-A.
PD 15-NOV-1995.
PF 02-NOV-1994; 002038.
PR 02-NOV-1994; AT-002038.
PA (BIOM-) BIOMAY PRODN & HANDELSGES MBH.
PI Achatz G, Breitenbach M, Ebner C, Kraft D, Lechenauer E;
PI Oberkofler H, Prillinger H, Simon B, Unger A;
DR WPI; 96-040555/05.
PT Recombinant DNA encoding allergens of Alternaria alternata - useful
PT in diagnosis and treatment of A. alternata allergies
PS Claim 1; Page 11; 21pp; German.
CC R8681-91 are T-cell epitopes derived from the Alt a 45 allergen protein
CC (R86872) isolated from Alternaria alternata. Peptide epitopes from Alt a
CC 45 and Alt a 12 (R86892) are useful as diagnostic reagents, e.g. for in
CC vitro detection of allergy caused by Alt a 45 and 12 (by reaction with
CC IgE in serum). They can also detect cellular reaction to the specified
CC allergens (from their stimulatory or inhibitory effect on this reaction).
CC The peptides can also be used therapeutically to induce immunotolerance
CC or anergy of T lymphocytes.
SQ Sequence 14 AA;

Query Match 60.0%; Score 21; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDL 6
DB 3 TEDDM 7

RESULT 29
W81217
ID W81217 standard; peptide; 6 AA.
AC W81217;
DE 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5246.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 6 /note= "Asp residue amidated"
FT W09845710-Al.
PN 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.

Query Match 60.0%; Score 21; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
DB 4 VTKDTLE 10

RESULT 28
W30922
ID W30922 standard; peptide; 14 AA.
AC W30922;
DE 08-JAN-1998 (first entry)
DE Birch pollen allergen B cell epitope.
DE Cofactor-independent phosphoglycerate mutase; PGM-i; E.C. 5.4.2.1;
KW Birch; pollen; allergy; plant allergen; panallergen; B cell;
KW T cell; epitope; immunotherapy; detection; diagnosis;
KW hay fever; conserved.
OS Betula verrucosa.
PN W09705258-A2.
PD 13-FEB-1997.
PF 02-AUG-1996; AT0141.
PR 02-AUG-1995; AT-001320.
PA (BIOM-) BIOMAY PRODN & HANDELS GMBH.
PI Breitenbach M, Ebner C, Engel E, Ferreira F, Jilek A;
PI Kraft D, Richter K, Rheinberger H;
DR WPI; 97-145695/13.
PT New recombinant DNA encoding plant phosphoglycerate mutase or its
PT antigenic epitope(s) - useful for diagnosis or treatment of
PT allergies to pollen and plant-derived foods
PS Disclosure; Fig 3; 160pp; German.
CC W30920-W30935 are B cell epitopes of a birch pollen co-factor-independent
CC phosphoglycerate mutase (PGM-i) allergen. PGM-i is a highly conserved
CC plant allergen (panallergen) which can cause cross-reactivity in
CC patients allergic to pollen and plant-derived foods. PGM-i and it's B
CC cell and T cell epitopes can be used for the in vitro detection of
CC allergy against PGM-i, by measuring serum IgE or a cellular reaction.
CC They can also be used in immunotherapy and will not cause an autoimmune
CC response because PGM-i is significantly different from the human
CC enzyme, which is co-factor dependent.
SQ Sequence 14 AA;

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PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 34; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 6 AA;

Query Match 57.1%; Score 20; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
Db 3 VTQD 6

RESULT 30
W81230
ID W81230 standard; peptide; 6 AA.
AC W81230;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5268.
KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified_site 6 /note= "Asp residue amidated"
PN WC9845710-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R;
DR WPI: 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 36; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 6 AA;

Query Match 57.1%; Score 20; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
Db 3 VTQD 6

Search completed: June 30, 2000, 14:52:32
Job time: 5999 sec

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OM protein - protein search, using sw model

Run on: June 30, 2000, 13:27:55 ; Search time 50.08 Seconds

(without alignments)
8.195 Million cell updates/sec

Title: US-08-833-506C-89

Perfect score: 35

Sequence: 1 VTQDDLQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 2577

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : PIR_63:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	60.0	7	2 S68004	hucolin, 75K chain
2	20	57.1	12	2 I39390	acetylcholine rece
3	20	57.1	15	2 E56819	PS I complex subun
4	20	57.1	15	2 A53594	calnexin - mouse (
5	19	54.3	11	2 S42449	anti protein - pha
6	18	51.4	12	2 B58503	outer membrane por
7	18	51.4	14	2 A61002	photosystem II oxy
8	17	48.6	13	2 A23694	myosin heavy chain
9	17	48.6	13	2 A57789	galbladder stone
10	17	48.6	15	2 PS0218	24K protein 4413 -
11	17	48.6	15	2 B48047	phospholipase C-be
12	16	45.7	8	2 I40697	biotin A - Citroba
13	16	45.7	4	3 PC4131	hypothetical 8 pro
14	16	45.7	11	2 PH0904	T-cell receptor be
15	16	45.7	12	2 S53681	yolk glycoprotein
16	16	45.7	12	2 S39762	cytochrome P450 Ut
17	16	45.7	13	2 S41209	F420-non-reducing-
18	16	45.7	13	2 PS0443	potassium channel
19	16	45.7	14	2 S29789	hypothetical prote
20	16	45.7	15	2 PA0110	translation elonga
21	16	45.7	15	2 B32800	hypothetical prote
22	16	45.7	15	2 C32521	hexokinase (EC 2.7
23	16	45.7	15	2 B26501	lipoprotein lipase
24	15	42.9	9	2 PW0002	chlorophyll a/b-bi
25	15	42.9	10	2 S13224	virG protein - Agr
26	15	42.9	13	2 S15755	actin 7 - soybean
27	15	42.9	14	2 A41589	25K elastin-bindin
28	15	42.9	14	2 I49514	B144 protein A - m
29	15	42.9	15	2 I58116	Dpil6 - human
30	15	42.9	15	2 PH1310	Ig heavy chain DJ

31	15	42.9	15	2 S31219	30K protein - bovi
32	15	42.9	15	2 A42413	Ig heavy chain V r
33	14	40.0	6	2 JH0784	neuropeptide TE-6
34	14	40.0	7	2 S16365	opacity protein P.
35	14	40.0	7	2 B39040	calsequestrin, fas
36	14	40.0	8	2 A61328	trypsin (EC 3.4.21
37	14	40.0	8	3 PQ0726	unidentified 4.5/4
38	14	40.0	10	2 I44644	neurotoxin-associa
39	14	40.0	11	2 S35490	type II site-speci
40	14	40.0	11	2 PS0257	31k protein 3208 -
41	14	40.0	11	2 A61512	variant surface gl
42	14	40.0	11	2 G42762	multicatalytic end
43	14	40.0	13	2 S44387	heat-shock protein
44	14	40.0	14	2 S17766	beta-glucosidase (
45	14	40.0	14	2 PH1768	T cell receptor al
46	14	40.0	14	2 F48394	glycoprotein compo
47	14	40.0	14	2 A39703	tubulin beta-3 cha
48	14	40.0	15	2 PC4268	alpha-globulin - r
49	14	40.0	15	2 S29487	GTP-binding protei
50	14	40.0	15	2 I29501	fibriopeptide A -
51	14	40.0	15	2 PT0205	insulin-like growt
52	14	40.0	15	2 PH1631	Ig H chain V-D-J r
53	14	40.0	15	2 G35141	T-cell receptor de
54	14	40.0	15	2 A31902	bone acidic glycop
55	14	40.0	15	2 D54226	light-harvesting p
56	13	37.1	5	2 PT0601	T-cell receptor be
57	13	37.1	6	2 PT0533	T-cell receptor be
58	13	37.1	7	2 S19630	ribosomal protein
59	13	37.1	7	2 PT0628	T-cell receptor be
60	13	37.1	7	2 PT0576	T-cell receptor be
61	13	37.1	9	2 PT0562	T-cell receptor be
62	13	37.1	9	2 B30572	T-cell receptor be
63	13	37.1	9	2 PH0937	T-cell receptor be
64	13	37.1	10	2 A55784	fibroblast growth
65	13	37.1	10	2 C30572	T-cell receptor be
66	13	37.1	11	2 I41978	calliFMRamide 9 -
67	13	37.1	11	2 S34065	ornithine decarbox
68	13	37.1	11	2 A34243	H-lysophorin - Ja
69	13	37.1	12	2 S51737	T-cell receptor be
70	13	37.1	12	2 S04013	lignin peroxidase
71	13	37.1	13	2 S04014	lignin peroxidase
72	13	37.1	13	2 B61458	Ig kappa chain V-I
73	13	37.1	13	2 A61458	Ig kappa chain V-I
74	13	37.1	13	2 C61576	ribosomal protein
75	13	37.1	14	2 S50900	chlorophyll a/b-bi
76	13	37.1	14	2 PH1615	Ig H chain V-D-J r
77	13	37.1	14	2 E30572	T-cell receptor be
78	13	37.1	15	2 PN0629	integration host f
79	13	37.1	15	2 PA0093	ennatiin synthetas
80	13	37.1	15	2 PA0062	fumarate hydratase
81	13	37.1	15	2 PA0088	protein QF200051 -
82	13	37.1	15	2 PN0144	serine proteinase
83	13	37.1	15	2 I50503	agrin - electric r
84	13	37.1	15	2 PL0154	glycoprotein - log
85	13	37.1	15	2 S57584	T cell receptor V-
86	13	37.1	15	2 S62675	collagen type I -
87	13	37.1	15	2 E49037	Tcr delta chain V-
88	13	37.1	15	2 S08301	epidermal growth f
89	12	34.3	5	2 PT0679	T-cell receptor be
90	12	34.3	6	2 PC4127	hypothetical 6 pro
91	12	34.3	6	2 B35640	cerbellar degener
92	12	34.3	7	2 A12016	formylglycinamide
93	12	34.3	7	2 PT0722	T-cell receptor be
94	12	34.3	8	2 PT0557	T-cell receptor be
95	12	34.3	8	2 S29272	tocopherol-binding
96	12	34.3	8	2 S69165	ferredoxin a2 - Ja
97	12	34.3	9	2 B41978	calliFMRamide 2 -
98	12	34.3	9	2 C41978	calliFMRamide 3 -
99	12	34.3	9	2 PH0108	late G1-69 protein
100	12	34.3	10	1 GMROL2	leucosulfakinin-II

ALIGNMENTS

```

RESULT 1
S68004
C:Title: Hucolin, 75K chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68004
R:Edgar, P.F.
FEBS Lett. 375, 159-161, 1995
A:Title: Hucolin, a new corticosteroid-binding protein from human plasma with structural
A:Reference number: S68004; MUID:96087107
A:Accession: S68004
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <EDG>

Query Match 50.0%; Score 21; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 4 DDLQ 7

RESULT 2
I39390
C:Title: acetylcholine receptor (alternative exon 5b) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 30-May-1997
C:Accession: I39390
R:Mihovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros
Biochem. Biophys. Res. Commun. 197, 137-144, 1993
A:Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for
A:Reference number: I39390; MUID:94071933
A:Accession: I39390
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:L18973; NID:g441143; PID:g441144
C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 57.1%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
Db 6 VTQGVQ 12

RESULT 3
PS I complex subunit 8 - cucumber (fragment)
C:Species: Cucumis sativus (cucumber)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C:Accession: E56819
R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A:Reference number: A56819; MUID:91355209
A:Accession: E56819
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <IWA>
A>Note: sequence extracted from NCBI backbone (NCBI:P:58606)

Query Match 57.1%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
Db 10 VIQDD 14

RESULT 4
A53594
C:Title: calnexin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999
C:Accession: A53594
R:Lenter, M.; Vestweber, D.
J. Biol. Chem. 269, 12263-12268, 1994
A:Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin
A:Reference number: A53594; MUID:94216347
A:Accession: A53594
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LEN>
C:Keywords: endoplasmic reticulum; molecular chaperone

Query Match 57.1%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDL 6
Db 10 IIEDDL 15

RESULT 5
S42449
C:Title: anti protein - phage P7
C:Species: phage P7
C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
C:Accession: S42449
R:Citron, M.; Schuster, H.
Cell 62, 591-598, 1990
A:Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A:Reference number: S42448; MUID:90335968
A:Accession: S42449
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-11 <CT>
A:Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 54.3%; Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6
Db 6 VTRNDI 11

RESULT 6
B58503
C:Title: outer membrane porin protein OprD homolog - unidentified bacterium (fragment)
N:Alternate names: 43K bile stone protein
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58503
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58503
A>Status: preliminary
A:Molecule type: protein
```

A:Residues: 1-12 <BIN>
A:Experimental source: human bile with stones
A:Note: sequenced along with secondary sequence MXIGVNEXL

Query Match 51.4%; Score 18; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDD 5
: : : :
Db 2 SQDD 5

RESULT 7
A61002
Photosystem II oxygen-evolving complex protein 1 - common tobacco (fragment)
N:Alternate names: thylakoid membrane protein
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
A:Accession: A61002
R:Baum, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C
Electrophoresis 11, 538-536, 1990
A:Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencing
A:Reference number: A61002; MUID:91031404
A:Accession: A61002
A:Molecule type: protein
A:Residues: 1-14 <BAU>
C:Keywords: Chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 51.4%; Score 18; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDIQ 7
: : : : :
Db 7 LTFDEIQ 13

RESULT 8
A23694
Myosin heavy chain, smooth muscle - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 07-Feb-1997
C:Accession: A23694
R:Cote, D.G.; Yount, R.G.
J. Biol. Chem. 265, 22537-22546, 1990
A:Title: Photolabeling of the 6 and 10 S conformations of gizzard myosin with 3'-(2')-O-(
A:Reference number: A23694; MUID:91093105
A:Accession: A23694
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <COL>
C:Keywords: smooth muscle

Query Match 48.6%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDD 5
: : : :
Db 11 QDD 13

RESULT 9
A57789
gallbladder stone matrix protein 1, 41K - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
A:Accession: A57789
R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996
A:Description: The proteins of gallbladder stones.
A:Reference number: A57789
A:Accession: A57789
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BIN>
A:Experimental source: two gallbladder, one bladder, one kidney stone of different pa
A:Note: 9-Leu and 12-Lys were also found

Query Match 48.6%; Score 17; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDD 5
: : : :
Db 3 QDD 5

RESULT 10
PS0218
24K protein 4413 - rice (strain Nihonbare) (fragment)
N:Alternate names: unidentified protein QR310029
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Aug-1997
A:Accession: PS0218; PC4270
R:Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0218
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: strain Nihonbare
R:Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A:Reference number: PC4267
A:Accession: PC4270
A:Molecule type: protein
A:Residues: 1-15 <RAW>

Query Match 48.6%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
: : : :
Db 1 LTQD 4

RESULT 11
B48047
phospholipase C-beta 4, PLC-beta - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: B48047
R:Lee, C.W.; Park, D.J.; Lee, K.H.; Kim, C.G.; Rhee, S.G.
J. Biol. Chem. 268, 21318-21327, 1993
A:Title: Purification, molecular cloning, and sequencing of phospholipase C-beta 4.
A:Reference number: A48047; MUID:94012887
A:Accession: B48047
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LEE>
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBIP:138522)

Query Match 48.6%; Score 17; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
| | : | |
Db 3 VTVEDEQ 9

RESULT 12
I40697
biotin A - Citrobacter freundii (fragment)
C:Species: Citrobacter freundii
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C:Accession: I40697
R:Shiuan, D.; Campbell, A.
Gene 67, 203-211, 1988
A:Title: Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter
A:Reference number: I40697; MUID:89006280
A:Accession: I40697
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:M21922; NID:g144434

Query Match 45.7%; Score 16; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODD 5
| | |
Db 1 TTDD 4

RESULT 13
PC41131
hypothetical 8 protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 03-Sep-1998 #sequence_revision 03-Sep-1998 #text_change 03-Sep-1998
C:Accession: PC41131
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Sequencing and characterization of the downstream region of the genes encoding
Y for biosynthesis of heme d1
A:Reference number: JC4552; MUID:96144254
A:Accession: PC41131
A>Status: preliminary
A:Residues: 1-8 <KAW>
A:Cross-references: DBJ:D50473

Query Match 45.7%; Score 16; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
| | |
Db 2 DDL 4

RESULT 14
PH0904
T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0904
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857
A:Accession: PH0904
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: myelin basic protein-immunized T-cell
C:Keywords: T-cell receptor

Query Match 45.7%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
: | | |
Db 3 SDSLQ 8

RESULT 15
S55681
yolk glycoprotein 42k - chicken
C:Species: Gallus gallus (chicken)
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55681
R:Yamamura, J.; Adachi, T.; Aoki, N.; Nakajima, H.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1244, 384-394, 1995
A:Title: Precursor-product relationship between chicken vitellogenin and the yolk pro
A:Reference number: S55680; MUID:95322425
A:Accession: S55681
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <YAM>
C:Keywords: glycoprotein

Query Match 45.7%; Score 16; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
: | |
Db 7 IQAED 11

RESULT 16
S39762
cytochrome P450 UT-7b - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C:Accession: S39762
R:Ohishi, N.; Imaoka, S.; Suzuki, T.; Funae, Y.
Biochim. Biophys. Acta 1158, 227-236, 1993
A:Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
A:Reference number: S39761; MUID:94072607
A:Accession: S39762
A:Molecule type: protein
A:Residues: 1-12 <OHI>

Query Match 45.7%; Score 16; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
| | |
Db 6 DDL 8

RESULT 17
S41209
F420-non-reducing-hydrogenase (EC 1.12.99.-) 17K chain - Methanobacterium thermoautot
C:Species: Methanobacterium thermoautotrophicum
A:Variety: Strain Marburg
C:Date: 06-Feb-1995 #sequence_revision 17-Jul-1998 #text_change 07-May-1999
C:Accession: S41209
R:Setzke, E.; Hedderich, R.; Heiden, S.; Thauer, R.K.
Eur. J. Biochem. 220, 139-148, 1994
A:Title: H(2): heterodisulfide oxidoreductase complex from Methanobacterium thermoaut
A:Reference number: S41204; MUID:94164153

A:Accession: S41209
A:Molecule type: protein
A:Residues: 1-13 <SET>
A:Experimental source: strain Marburg
C:Complex: membrane-associated complex; holoenzyme is the hydrogen:heterodisulfide oxidoreductase (EC 1.12.99.2) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.2)
A:Description: reduction of coenzyme M-N-7-mercaptoheptanoylthreosine phosphate heterodisulfide (EC 1.12.99.2)
C:Keywords: membrane-associated complex; oxidoreductase

Query Match 45.7%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDDL 6
DB 2 EDDI 5

RESULT 18
PS0443
potassium channel protein Slo G3 - fruit fly (*Drosophila melanogaster*) (fragment)
C:Species: *Drosophila melanogaster*
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C:Accession: PS0443
R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992

A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A:Reference number: JH0697; MUID:92360298
A:Accession: PS0443
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-13 <ADE>
C:Comment: This potassium channel is activated by calcium.
C:Genetics:
A:Gene: FlyBase:slo
A:Cross-references: FlyBase:FBgn0003429
C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 45.7%; Score 16; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 10 DDL 12

RESULT 19
S29789
hypothetical protein - Thermoplasma acidophilum (fragment)
C:Species: *Thermoplasma acidophilum*
C>Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: S29789
R:Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Towner, P.
Eur. J. Biochem. 211, 549-554, 1993
A:Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenase from *Thermoplasma acidophilum*
A:Reference number: S29788; MUID:93170285
A:Accession: S29789
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <BRI>
A:Cross-references: EMBL:X59788

Query Match 45.7%; Score 16; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6

DB 9 DDL 11

RESULT 20

PA0110
translation elongation factor eEF-1 beta' chain - *Arabidopsis thaliana* (fragment)
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 26-Apr-1996
C:Accession: PA0110
R:Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0109
A:Accession: PA0110
A:Molecule type: protein
A:Residues: 1-15 <RAW>

Query Match 45.7%; Score 16; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTODDL 6
DB 2 VTFSDL 7

RESULT 21

B32800
hypothetical protein (p1 5' region) - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 30-Sep-1993
C:Accession: B32800
R:Jindal, S.; Dudani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.
Mol. Cell. Biol. 9, 2279-2283, 1989
A:Title: Primary structure of a human mitochondrial protein homologous to the bacteriophage T4 gp105
A:Reference number: A32800; MUID:89313783
A:Accession: B32800
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <JIN>
A:Cross-references: GB:M22382

Query Match 45.7%; Score 16; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 1 DDL 3

RESULT 22

C32521
hexokinase (EC 2.7.1.1) I peptide II - rat (fragment)
C:Species: *Rattus norvegicus* (Norway rat)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 28-Apr-1993
C:Accession: C32521
R:Schirch, D.M.; Willson, J.E.
Arch. Biochem. Biophys. 257, 1-12, 1987
A:Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site
A:Reference number: A90080; MUID:87324917
A:Accession: C32521
A:Molecule type: protein
A:Residues: 1-15 <SCH>
C:Keywords: glycolysis; phosphotransferase

Query Match 45.7%; Score 16; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODD 5
| | |
Db 11 TXDD 14

RESULT 23

B26501
lipoprotein lipase (EC 3.1.1.34) - guinea pig (fragment)

C:Species: Cavia porcellus (guinea pig)

C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 28-Apr-1993

C:Accession: B26501

R:Bengtsson-Oliverona, G.; Oliverona, T.; Jorvall, H.

Eur. J. Biochem. 161, 281-288, 1986

A:Title: Lipoprotein lipases from cow, guinea-pig and man. Structural characterization a

A:Reference number: A91178; MUID:87034027

A:Accession: B26501

A:Molecule type: protein

A:Residues: 1-15 <BEN>

C:Keywords: carboxylic ester hydrolase

Query Match

Best Local Similarity 45.7%; Score 16; DB 2; Length 15;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7

| | |

Db 8 DDIE 11

RESULT 24

PW0002

chlorophyll a/b-binding protein 31k - green alga (Dunaliella tertiolecta) (fragment)

N:Alternate names: photosystem II light-harvesting chlorophyll 31K protein

C:Species: Dunaliella tertiolecta

C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999

C:Accession: PW0002

R:LaRoche, J.; Bennett, J.; Falkowski, P.G.

Gene 95, 165-171, 1990

A:Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the

A:Reference number: JW0040; MUID:91065528

A:Accession: PW0002

A:Molecule type: protein

A:Residues: 1-9 <LAK>

C:Superfamily: chlorophyll a/b-binding protein

C:Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match

Best Local Similarity 42.9%; Score 15; DB 2; Length 9;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7

| | |

Db 4 DEMQ 7

RESULT 25

S13224

virG protein - Agrobacterium sp. (fragment)

C:Species: Agrobacterium sp.

C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997

C:Accession: S13224

R:Tamamoto, S.; Aoyama, T.; Takanami, M.; Oka, A.

J. Mol. Biol. 215, 537-547, 1990

A:Title: Binding of the regulatory protein VirG to the phased signal sequences upstream

A:Reference number: S13224; MUID:91039316

A:Accession: S13224

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <TAM>

Query Match 42.9%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTODD 5

| | |

Db 6 VIDDD 10

RESULT 26

S15755

actin 7 - soybean (fragment)

C:Species: Glycine max (soybean)

C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 13-Aug-1999

C:Accession: S15755

R:Pearson, L.; Meagher, R.B.

Plant Mol. Biol. 14, 513-526, 1990

A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untransla

A:Reference number: S15754; MUID:91346640

A:Accession: S15755

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <PEA>

A:Cross-references: EMBL:X17120; NID:g18527; PIDN:CAA34980.1; PID:g18528

C:Superfamily: actin

C:Keywords: cytoskeleton; structural protein

Query Match

Best Local Similarity 42.9%; Score 15; DB 2; Length 13;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7

| | |

Db 5 EDIQ 8

RESULT 27

A41589

25K elastin-binding protein - Staphylococcus aureus (fragment)

C:Species: Staphylococcus aureus

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Mar-1993

C:Accession: A41589

R:Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.;

J. Biol. Chem. 266, 23399-23406, 1991

A:Title: Binding of elastin to Staphylococcus aureus.

A:Reference number: A41589; MUID:92078218

A:Accession: A41589

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <PAR>

Query Match

Best Local Similarity 42.9%; Score 15; DB 2; Length 14;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QDDLQ 7

| | |

Db 5 KDDFE 9

RESULT 28

I49514

B144 protein A - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49514

R:Tsuge, I.; Shen, F.

Immunogenetics 26, 378-380, 1987

A:Title: A gene in the H-2S: H-2D interval of the major histocompatibility complex wh

A:Reference number: I49514; MUID:88031493

A:Accession: I49514

A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-14 <RES>
A:Cross-references: GB:M18187; NID:g192097; PIDN:AAA37272.1; PID:g192098

Query Match 42.9%; Score 15; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7
| | |
Db 3 DLQ 5

RESULT 29
I58116
Dp116 - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I58116
R:Byers, T.J.; Lidov, H.G.; Kunkel, L.M.
Nature Genet. 4, 77-81, 1993
A:Title: An alternative dystrophin transcript specific to peripheral nerve.
A:Reference number: I58116; MUID:93291881
A:Accession: I58116
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-15 <RES>
A:Cross-references: GB:S62617; NID:g386224; PIDN:AAB27159.1; PID:g386225
C:Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin

Query Match 42.9%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7
| | |
Db 11 DLQ 13

RESULT 30
PH1310
Ig heavy chain DJ region (clone C770-107) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1310
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761
A:Accession: PH1310
A:Molecule type: DNA
A:Residues: 1-15 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 15; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDL 6
| | |
Db 1 TQDEL 5

Search completed: June 30, 2000, 14:54:15
Job time: 5180 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:52:37 ; Search time 39.08 Seconds
(without alignments)
5.455 Million cell updates/sec

Title: US-08-833-506c-89
Perfect score: 35
Sequence: 1 VTQDDIQ 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 668

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	57.1	15	PSAO_CUCSA	P42052 cucumis sat
2	17	48.6	5	BIOA_CITFR	P13071 citrobacter
3	17	48.6	5	BIOA_SALTY	P12677 salmoneilla
4	17	48.6	9	UF02_MOUSE	P38640 mus musculus
5	16	45.7	12	XYLA_STRVN	P14405 streptomyce
6	16	45.7	14	YGBH_TREAC	Q05213 thermoplas
7	15	42.9	11	UF05_MOUSE	P38643 mus musculus
8	15	42.9	13	ACT7_SOYBN	P15987 glycine max
9	15	42.9	14	GLGS_SPIOL	P55235 spinacia ol
10	14	40.0	10	UXA7_CHLTR	P38008 chlamydia t
11	14	40.0	11	T2P1_PROVU	P31031 proteus vul
12	14	40.0	12	UP01_CAEEL	P55954 caenorhabdi
13	14	40.0	13	UN02_PINPS	P81667 pinus pinas
14	14	40.0	14	RECJ_SALTY	P28355 salmoneilla
15	14	40.0	15	FR57_PINPS	P81104 pinus pinas
16	13	37.1	11	FAR9_CALVO	P41864 calliphora
17	13	37.1	12	LOSK_LOEMI	P47733 locusta mig
18	13	37.1	12	ULAL_MOUSE	P99032 mus musculus
19	13	37.1	13	EP65_HUMAN	P54963 homo sapien
20	13	37.1	13	LIGA_TRAVE	P20011 trameetes ve
21	13	37.1	13	LIGB_TRAVE	P20012 trameetes ve
22	13	37.1	14	RL30_SALTY	Q54300 salmoneilla
23	13	37.1	14	HCYA_MEGCR	Q10583 megathura c
24	13	37.1	15	ITRB_ALBUJ	P24927 albizzia ju
25	13	37.1	15	IRKG_CARCR	P21586 caretta car
26	13	37.1	15	UN01_PINPS	P81106 pinus pinas
27	12	34.3	9	FAR2_CALVO	P41857 calliphora
28	12	34.3	9	FAR3_CALVO	P41858 calliphora
29	12	34.3	9	NSK1_SARBU	P41492 sarcophaga
30	12	34.3	9	UHA2_HUMAN	P40929 homo sapien
31	12	34.3	9	UTAH_HUMAN	P31934 homo sapien
32	12	34.3	10	FARC_CALVO	P41867 calliphora
33	12	34.3	10	FIBB_CERSI	P14537 ceratotheri
34	12	34.3	10	GS09_BACSU	P80243 bacillus su

35	12	34.3	10	LSK2_LEUMA	P09039 leucophaea
36	12	34.3	10	UPA2_HUMAN	P30088 homo sapien
37	12	34.3	11	LSRP_PERAM	P3685 periplaneta
38	12	34.3	11	RR2_CONAM	P4341 conopholis
39	12	34.3	11	RRPL_CHAV	P13179 chandipura
40	12	34.3	12	CALM_TETTH	Q05055 tetrahymena
41	12	34.3	13	FIBB_RABIT	P14478 oryctolagus
42	12	34.3	13	ODPA_CANFA	P49823 canis famill
43	12	34.3	13	UN10_CLOPA	P81345 clostridium
44	12	34.3	14	LECB_PSOSC	P2584 psophocarpu
45	12	34.3	14	MARI_ALTSP	P29399 alteromonas
46	12	34.3	14	NSK2_SARBU	P41493 sarcophaga
47	12	34.3	14	TKNM_RANMA	P40951 rana margar
48	12	34.3	15	48KD_BACCE	P80173 bacillus ce
49	12	34.3	15	UC28_WAIZE	P80634 zea mays (m
50	11	31.4	8	CLP_THICU	P80488 thlobacilli
51	11	31.4	9	DI_NEPNO	P24816 nephrops no
52	11	31.4	9	DCML_PSECF	P19913 pseudomonas
53	11	31.4	9	FAR1_CALVO	P41856 calliphora
54	11	31.4	9	FAR4_CALVO	P41859 calliphora
55	11	31.4	9	FAR5_CALVO	P41860 calliphora
56	11	31.4	9	FAR6_CALVO	P41861 calliphora
57	11	31.4	9	FAR7_CALVO	P41862 calliphora
58	11	31.4	9	FARD_CALVO	P41868 calliphora
59	11	31.4	9	LMTP_LOEMI	P31799 locusta mig
60	11	31.4	10	CAER_LITXA	P56264 litoria xan
61	11	31.4	10	FARP_WANSE	P18223 manduca sex
62	11	31.4	10	LCNS_LEUMA	P21144 leucophaea
63	11	31.4	10	SPI_HALRO	Q10997 halocynthia
64	11	31.4	10	UH05_RAT	P56573 rattus norv
65	11	31.4	10	XYNB_DICBA	P80717 dictyoglomu
66	11	31.4	13	GER1_HORVU	P28525 hordeum vul
67	11	31.4	13	GER2_HORVU	P28526 hordeum vul
68	11	31.4	13	PSAJ_PEA	P17229 pisum sativ
69	11	31.4	14	LPW_RHIME	P18854 rhizobium m
70	11	31.4	14	CY56_CLOPA	P81362 clostridium
71	11	31.4	15	FIBA_ANAPL	P13401 andas piatyr
72	11	31.4	15	MAOX_CHICK	Q92060 gallus gall
73	11	31.4	15	PKRH_PHPYA	P80659 physcomitre
74	11	31.4	15	PGTS_PELAC	P80564 pelobacter
75	11	31.4	15	TERM_BPM2	P19897 bacterioph
76	11	31.4	15	TRPI_PSEPU	P36414 pseudomonas
77	10	28.6	6	FIBB_PAPAN	P19344 papio anubi
78	10	28.6	9	FIBB_PAPHA	P19343 papio hamad
79	10	28.6	9	FIBB_THEGE	P19342 theropithe
80	10	28.6	10	COXA_ONCMY	P80328 oncorhynch
81	10	28.6	10	MALE_KLEPN	Q05564 klebsiella
82	10	28.6	10	MOSQ_CLYTA	P19962 clypeaster
83	10	28.6	11	TRNI_OPERU	P08612 uperoleia r
84	10	28.6	11	TCRB_MEGCR	Q10584 megathura c
85	10	28.6	12	TKN_KASSE	P08511 kassina sen
86	10	28.6	12	UCRH_MOUSE	P99028 mus musculus
87	10	28.6	12	UR2_GILMI	P01147 gillichthys
88	10	28.6	12	ECDE_LYMDI	P80941 lymantria d
89	10	28.6	13	IDHC_FIG	P20304 sus scrofa
90	10	28.6	13	LPAA_PORGI	P81411 porphyromon
91	10	28.6	13	ORCK_ORCLI	P37086 orconectes
92	10	28.6	13	PRC_SALTY	P43669 salmoneilla
93	10	28.6	13	SODM_CANFA	P54712 canis famill
94	10	28.6	13	UHA1_HUMAN	P40928 homo sapien
95	10	28.6	13	UN12_CLOPA	P81353 clostridium
96	10	28.6	14	ALYT_ALYOC	P08944 alytes obst
97	10	28.6	14	DHSL_ANACY	P17874 anabaena cy
98	10	28.6	14	GR75_CANFA	P99502 canis famill
99	10	28.6	14	SODN_STRCO	P80735 streptomyce
100	10	28.6	14		

ALIGNMENTS

RESULT 1
PSNO_CUCSA

```

ID PSNO_CUCSA STANDARD; PRT; 15 AA.
AC P42052;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PHOTOSYSTEM 1 REACTION CENTRE SUBUNIT 8 (PHOTOSYSTEM I 17.5 KD
DE PROTEIN) (FRAGMENT).
PSAM.
GN Cucumis sativus (Cucumber).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
OC Cucumis.
RN [1]
RP SEQUENCE.
RC TISSUE=COTYLEDON;
RX MEDLINE; 91355209.
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I
RT complex by N-terminal sequencing."
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -!- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.
KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid membrane.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;

Query Match 57.1%; Score 20; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 10 VIQDD 14

RESULT 2
BIOA_CITFR STANDARD; PRT; 5 AA.
ID BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
DE (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
DE AMINOTRANSFERASE) (FRAGMENT).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89006280.
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
CC OXONONANOATE -> S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
CC 7,8-DIAMINONONANOATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: BIOTIN BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
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CC
CC EMBL; M21922; CAB25119.1; -.
DR STYGNE; SG10026; BIOA.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 8.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 1 MTTDD 5

RESULT 3
BIOA_SALTY STANDARD; PRT; 5 AA.
ID BIOA_SALTY STANDARD; PRT; 5 AA.
AC P12677;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE
DE (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA
DE AMINOTRANSFERASE) (FRAGMENT).
GN BIOA.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89006280.
RA Shuan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-
CC OXONONANOATE -> S-ADENOSYL-4-METHYLTHIO-2-OXOBUTANOATE +
CC 7,8-DIAMINONONANOATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- PATHWAY: BIOTIN BIOSYNTHESIS.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
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CC
CC EMBL; M21922; CAB25119.1; -.
DR STYGNE; SG10026; BIOA.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON_TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 48.6%; Score 17; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 8.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 1 MTTDD 5
```

```
RESULT 4
UF02_MOUSE STANDARD; PRT; 9 AA.
AC P38640;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P32) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC TISSUE=FIBROBLAST;
RX MEDLINE; 95009907.
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 32 KD.
FT NON_TER 9
FT SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 48.6%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 8.4e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDDIQ 7
DB 2 EDEIQ 6

RESULT 5
XYLA_STRVN STANDARD; PRT; 12 AA.
AC P14405;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE XYLOSE ISOMERASE (EC 5.3.1.5) (FRAGMENT).
OS Streptomyces violaceoruber.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE.
RC STRAIN=LMG 7183;
RX MEDLINE; 90104230.
RA Vangrype W., Ampe C., Kersters-Hilderson H., Tempst P.;
RT "Single active-site histidine in D-xylose isomerase from Streptomyces
RT violaceoruber. Identification by chemical derivatization and peptide
RT mapping.";
RL Biochem. J. 263:195-199(1989).
CC -1- CATALYTIC ACTIVITY: D-XYLOSE -> D-XYLULOSE.
CC -1- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
DR HSP: P37031; 1DXI.
DR PROSITE; PS00172; XYLOSE ISOMERASE_1; PARTIAL.
DR PROSITE; PS00173; XYLOSE ISOMERASE_2; PARTIAL.
KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
FT NON_TER 1
FT ACT_SITE 5
FT NON_TER 5
FT NON_TER 12
FT SEQUENCE 12 AA; 1375 MW; E749268EB1AAAAA1 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 DDL 6
DB 7 DDL 9

RESULT 6
YGDH_THEAC STANDARD; PRT; 14 AA.
ID YGDH_THEAC
AC Q05213;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE HYPOTHETICAL PROTEIN IN GLUCOSE DEHYDROGENASE GENE 3'REGION
DE (FRAGMENT).
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;
OC Thermoplasma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE; 93170285.
RA Bright J.R., Byrom D., Danson M.J., Hough D.W., Towner P.;
RT "Cloning, sequencing and expression of the gene encoding glucose
RT dehydrogenase from the thermophilic archaeon Thermoplasma
RT acidophilum.";
RT Eur. J. Biochem. 211:549-554(1993).
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CC -----
DR EMBL; X59788; CAA42451.1; -
DR PIR; S29789; S29789.
KW Hypothetical protein.
FT NON_TER 14
FT SEQUENCE 14 AA; 1674 MW; 685A1FFF26529944 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 9 DDL 11

RESULT 7
UF05_MOUSE STANDARD; PRT; 11 AA.
ID UF05_MOUSE
AC P38643;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P48) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC TISSUE=FIBROBLAST;
RX MEDLINE; 95009907.
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 48 KD.
```

```
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAABAF6A CRC64;

Query Match 42.9%; Score 15; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.7e+02;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQDDL 6
   : ||:
Db 3 IXXDDV 8

RESULT 8
ACT7_SOYBN STANDARD; PRT; 13 AA.
AC P15987:
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 13-JUL-1999 (Rel. 38, Last annotation update)
DE ACTIN 7 (FRAGMENT).
GN SAC7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Glycine.
OC [1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV WAYNE.
RX MEDLINE; 91346640.
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -1- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC -----
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CC -----
CC EMBL: X17120; CAA34980.1; -.
CC PIR: S15755; S15755.
CC DR PROSITE; PS00406; ACTINS.1; PARTIAL.
CC DR PROSITE; PS00432; ACTINS.2; PARTIAL.
CC DR PROSITE; PS01132; ACTINS.ACT-LIKE; PARTIAL.
CC KW Structural protein; Multigene family.
CC NON_TER 13 13
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 42.9%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDQ 7
   : ||:
Db 5 EDIQ 8

us-08-833-506c-89.shoert.rsp
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RESULT 9
GLGS_SPIOL STANDARD; PRT; 14 AA.
AC P55235;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT (EC 2.7.7.27)
DE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B)
DE (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (FRAGMENT).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Caryophyllales; Caryophyllales; Chenopodiaceae;
OC Spinacia.
OC [1]
RN SEQUENCE.
RP TISSUE-LEAF;
RA Morell M.K., Bloom M., Knowles V., Preiss J.;
RT "Subunit structure of spinach leaf ADPglucose pyrophosphorylase.";
RL Plant Physiol. 85:182-187(1987).
CC -1- FUNCTION: THIS PROTEIN PLAYS A ROLE IN SYNTHESIS OF STARCH.
CC IT CATALYZES THE SYNTHESIS OF THE ACTIVATED GLYCOSYL DONOR,
CC ADP-GLUCOSE FROM GLC-1-P AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + ALPHA-D-GLUCOSE 1-PHOSPHATE =
CC PYROPHOSPHATE + ADP-GLUCOSE.
CC -1- ENZYME REGULATION: ACTIVATED BY 3'PHOSPHOGLYCERATE, INHIBITED
CC BY ORTHOPHOSPHATE. ALLOSTERIC REGULATION.
CC -1- PATHWAY: STARCH BIOSYNTHESIS.
CC -1- SUBUNIT: HETEROTETRAMER.
CC -1- SUBCELLULAR LOCATION: CHLOROPLASTS OF LEAVES AND AMYLOPLASTS
CC OF DEVELOPING ENDOSPERM.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL AND PLANTS GLUCOSE-1-
CC PHOSPHATE ADENYLYLTRANSFERASE FAMILY.
CC PROSITE; PS00808; ADP_GLC_PYROPHOSPH_1; PARTIAL.
CC PROSITE; PS00809; ADP_GLC_PYROPHOSPH_2; PARTIAL.
CC PROSITE; PS00810; ADP_GLC_PYROPHOSPH_3; PARTIAL.
CC KW Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
CC Multigene family; Starch biosynthesis; Allosteric enzyme;
CC Amyloplast; Chloroplast.
CC NON_TER 14 14
SQ SEQUENCE 14 AA; 1490 MW; 98B5792C3AE738C5 CRC64;

Query Match 42.9%; Score 15; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TQDDL 6
   : ||:
Db 7 SQDGL 11

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RESULT 10
UXAV_CHLTR STANDARD; PRT; 10 AA.
AC P38008;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OC [1]
RN SEQUENCE.
RP STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magl B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.65 OR 6.89 (TWO SPOTS ARE PRESENT), ITS MW IS: 70
CC KD.
```

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FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1251 MW; 80A43FD6D731AAB1 CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DDLQ 7
DB 4 DTLQ 7

RESULT 11
T2PL_PROVU STANDARD; PRT; 11 AA.
AC P31031;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE TYPE II RESTRICTION ENZYME PVUI (EC 3.1.21.4) (ENDONUCLEASE PVUI)
DE (R. PVUI) (FRAGMENT).
OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13315;
RX MEDLINE; 93087186.
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the Pvui restriction and
modification system.";
RL Nucleic Acids Res 20:5743-5747(1992).
CC -!- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG
CC AND CLEAVES AFTER T-4.
CC -----
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CC -----
DR EMBL; L04163; AAA25660.1; -
DR PIR; S35490; S35490.
DR REBASE; RB00107; Pvui.
KW Hydrolase; Endonuclease; Nuclease; Restriction system.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 11;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTODDL 6
DB 1 ISVDEL 6

RESULT 12
UP01_CAEEL STANDARD; PRT; 12 AA.
AC P55954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 1) (FRAGMENT).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
```

```
RP SEQUENCE.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 97295299.
RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
RL Electrophoresis 18:557-562(1997).
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 12;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
DB 4 DDI 6

RESULT 13
UN02_PINPS STANDARD; PRT; 13 AA.
AC P81667;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N55) (FRAGMENTS).
OC Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE-NEEDLE;
RX MEDLINE; 99274088.
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- INDUCTION: BY WATER-STRESS.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 43 KD.
FT NON_TER 1 1
FT NON_CONS 7 8
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1559 MW; 966B5A43EF94B411 CRC64;

Query Match
Best Local Similarity 40.0%; Score 14; DB 1; Length 13;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TODDL 6
DB 6 TRDNV 10

RESULT 14
RECJ_SALTY STANDARD; PRT; 14 AA.
AC P28355;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1.-.-) (FRAGMENT).
GN RECJ.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
```

RX MEDLINE: 91046011.
RA Kawakami K., Nakamura Y.;
RT "Autogenous suppression of an opal mutation in the gene encoding
RL Peptide chain release factor 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8432-8436(1990).
CC -1- FUNCTION: SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE. REQUIRED FOR
CC MANY TYPES OF RECOMBINATIONAL EVENTS, ALTHOUGH THE STRINGENCY OF
CC THE REQUIREMENT FOR RECJ APPEARS TO VARY WITH THE TYPE OF
CC RECOMBINATIONAL EVENT MONITORED AND THE OTHER RECOMBINATION GENE
CC PRODUCTS WHICH ARE AVAILABLE.
CC -----
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CC -----
DR EMBL: M38590; AAA72913.1; -.
DR SYNGENE; SG10332; RECJ.
KW Hydrolase; Nuclease; Exonuclease.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1696 MW; 105E784AC26C5650 CRC64;

Query Match 40.0%; Score 14; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
Db 9 DDI 11

RESULT 15
FKB7_PINPS STANDARD; PRT; 15 AA.
AC P01104;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 38, Last annotation update)
DE 70 KD PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS
DE ISOMERASE) (CYCLOPHILIN) (PIASE) (S1205-06) (FRAGMENT).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Metazoa; Embryophyta; Tracheophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RA Plomion C., Costa P., Bahrman N., Frigerio J.-M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map.";
RL Silvae Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RX MEDLINE: 9274088.
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PEPTIDYLPROLINE (OMEGA=180) -
CC PEPTIDYLPROLINE (OMEGA=0).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.3, ITS MW IS: 72 KD.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR PROSITE; PS00453; FKBP_PPIASE_1; PARTIAL.
DR PROSITE; PS00454; FKBP_PPIASE_2; PARTIAL.

DR PROSITE; PS00509; FKBP_PPIASE_3; PARTIAL.
KW Isomerase; Rotamase; Repeat; Calmodulin-binding.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1675 MW; 2B53999722277F3F CRC64;

Query Match 40.0%; Score 14; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 2.2e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
Db 10 TGDEVE 15

RESULT 16
FAR9_CALVO STANDARD; PRT; 11 AA.
ID FAR9_CALVO
AC P41864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CALLIFMRFAMIDE 9.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.
RN [1]
RP SEQUENCE.
RC TISSUE=THORACIC GANGLION;
RX MEDLINE: 92196111.
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifmrfamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR: I41978; I41978.
KW Neuropeptide; Amidation.
FT MOD_RES 11
FT SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDD 5
Db 4 TKND 7

RESULT 17
LOSK_LOCFMI STANDARD; PRT; 12 AA.
ID LOSK_LOCFMI
AC P47733;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SULFAKININ (LOW-SK).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthoptera; Orthoptera; Caelifera;
OC Acridoidea; Acridoidea; Acrididae; Oedipodinae; Locusta.
RN [1]
RP SEQUENCE.
RC TISSUE=BRAIN;
RA Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
RL (In) McCaffery A., Wilson I. (eds.);
RL Chromatography and isolation of insect hormones and pheromones,

RL pp.231-241, Plenum Press, New York (1990).
CC -!- FUNCTION: MYOTROPIC PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amigation; Sulfatation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 7 7 SULFATATION (POTENTIAL).
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1440 MW; 9B5B5DA9BD6B5AAA CRC64;

Query Match 37.1%; Score 13; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 2 LASDD 6

RESULT 18
ID ULAL_MOUSE STANDARD; PRT; 12 AA.
AC P99032;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 2D-0014M9)
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC TISSUE=LIVER;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
RA Hooiland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 11.7 KD.
DR SWISS-2DPAGE; P99032; MOUSE.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1324 MW; DD6468EE9F75BAB6 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
DB 2 DNVQ 5

RESULT 19
ID EP65_HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ERYTHROCYTE 65 KD PROTEIN (P65) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE, AND CARBOHYDRATE-BINDING SITE.
RX MEDLINE; 90004678.
RA Hart G.W., Haitiwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins."; Ciba Found. Symp. 145:102-118(1989).
RL Ciba Found. Symp. 145:102-118(1989).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.

KW Glycoprotein. 1
FT NON_TER 1
FT CARBOHYD 2 O-LINKED (GLCNAC).
FT NON_TER 13
SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;
Query Match 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDDL 6
DB 4 VSQPSL 9

RESULT 20
ID LIGA_TRAVE STANDARD; PRT; 13 AA.
AC P20011;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LIGNINASE A (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;
OC Coriolaceae; Trametes.
RN [1]
RP SEQUENCE.
RX MEDLINE; 89211432.
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
RT "Trametes versicolor ligninase: isozyme sequence homology and substrate specificity"; FEBS Lett. 247:143-146(1989).
CC -!- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE C (ALPHA)-C (BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
CC -!- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.
DR PIR; S04013; S04013.
DR PROSITE; P500435; PEROXIDASE_1; PARTIAL.
DR PROSITE; P500436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family; Lignin degradation.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VTQDD 5
DB 1 VTXP 5

RESULT 21
ID LIGA_TRAVE STANDARD; PRT; 13 AA.
AC P20012;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE LIGNINASE B (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;
OC Coriolaceae; Trametes.
RN [1]
RP SEQUENCE.
RX MEDLINE; 89211432.
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
RT "Trametes versicolor ligninase: isozyme sequence homology and substrate specificity"; FEBS Lett. 247:143-146(1989).
RL FEBS Lett. 247:143-146(1989).

```
CC -|- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE
CC C/(ALPHA)-C(BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
CC -|- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.
DR PIR; S04014; S04014.
DR PROSITE; PS00435; PEROXIDASE_1; PARTIAL.
DR PROSITE; PS00436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;
KW Lignin degradation. 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1269 MW; 22C50ED5872A52C8 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTQD 5
Db 1 VTXP 5

RESULT 22
RL30_SALTY STANDARD; PRT; 13 AA.
AC O54300;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 50S RIBOSOMAL PROTEIN L30 (FRAGMENT).
GN RPSD.
OS Salmonella typhimurium
CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Salmonella.
CC [1]
RP SEQUENCE FROM N.A.
RA Bjorkman J., Hughes D., Andersson D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AJ223237; CAAL1206.1;
DR STYGENE; SG77777; RPMD.
DR PROSITE; PS00634; RIBOSOMAL_L30; PARTIAL.
KW Ribosomal protein.
FT INIT_MET 0 BY SIMILARITY.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1431 MW; 15A0A8F8E8B3C1A0 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQ 3
Db 6 ITQ 8

RESULT 23
HCYA_MEGCR STANDARD; PRT; 14 AA.
AC Q10583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
```

```
DE HEMOCYANIN A CHAIN (KLH-A) (FRAGMENT).
OS Megathura crenulata.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
OC Patellicidae; Megathura.
RN [1]
RP SEQUENCE.
RX MEDLINE; 96208935.
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional
RT characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -|- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
CC ARTHROPODS.
CC -|- SUBUNIT: DECAMERS AND DIDECAMERS.
CC -|- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -|- TISSUE SPECIFICITY: HEMOLYMPH.
CC -|- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Respiratory protein; Oxygen transport; Copper; Glycoprotein;
KW Hemolymph. 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1610 MW; 9CB61977014A99D5 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQD 4
Db 11 LTQE 14

RESULT 24
ITRB_ALBUJ STANDARD; PRT; 15 AA.
AC P24927;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE TRYPsin INHIBITOR B CHAIN (FRAGMENT).
OS Albizzia julibrissin (Silk tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Mimosoideae;
OC Albizzia.
CC [1]
RN SEQUENCE.
RP TISSUE=SEED;
RC MEDLINE; 80115605.
RX Odani S., Ono T., Ikenaka T.;
RA "Proteinase inhibitors from a mimosoideae legume, Albizzia
RT julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
RL J. Biochem. 86:1795-1805(1979).
CC -|- FUNCTION: INHIBITS TRYPsin AND ALPHA-CHYMOTRYPsin.
CC -|- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -|- SIMILARITY: TO BETA CHAINS OF SOME OTHER LEGUMINOUS KUNITZ-TYPE
CC INHIBITORS.
KW Serine protease inhibitor.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QDD 5
Db 11
```

Db 1 KDD 3

RESULT 25
RKG_CARC STANDARD; PRT; 15 AA.
ID RKG_CARC AC P21586;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 19, Last annotation update)
DE RATHKE'S GLAND GLYCOPROTEIN (FRAGMENT).
OS Carretta caretta (loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
OC Cryptodira; Chelonioidea; Cheloniidae; Carretta.
RN [1]
RP SEQUENCE.
RC TISSUE=RATHKE'S GLAND;
RX MEDLINE; 90075703.
RA Radhakrishna G., Chin C.C.Q., Wold F., Weldon P.J.;
RT "Glycoproteins in Rathke's gland secretions of loggerhead (Carretta caretta) and Kemp's ridley (Lepidochelys kempi) sea turtles.";
RL Comp. Biochem. Physiol. 94B:375-378(1989).
CC -!- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES, AS PREDATOR REPELLENTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE TURTLE SHELL.
CC -!- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY SEA TURTLE.
CC PIR; PLO154; PLO154.
DR Glycoprotein.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1477 MW; CC893BAAA1B1B5ED CRC64;

Query Match 37.1%; Score 13; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TODD 5
: ||
Db 1 SDD 4

RESULT 26
UNO1_PINPS STANDARD; PRT; 15 AA.
ID UNO1_PINPS AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (S1247/S1248) (N150/N151) (FRAGMENT).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping dominant and codominant protein markers assayed on diploid tissue, in a haploid-based genetic map.";
RL Silvae Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RX MEDLINE; 92274088.
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.5, ITS MW IS: 62 KD.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 37.1%; Score 13; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQ 3
: ||
Db 5 ITQ 7

RESULT 27
FAR2_CALVO STANDARD; PRT; 9 AA.
ID FAR2_CALVO AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CALLIFMRFAMIDE 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.
RN [1]
RP SEQUENCE.
RC TISSUE=THORACIC GANGLION;
RX MEDLINE; 92196111.
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated callifmrfa-mides) from the blowfly Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
CC PIR; B41978; B41978.
DR Neuropeptide; Amidation.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00599CAB6C5A7 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TOD 4
: ||
Db 3 SQD 5

RESULT 28
FAR3_CALVO STANDARD; PRT; 9 AA.
ID FAR3_CALVO AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CALLIFMRFAMIDE 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Calliphora.
RN [1]
RP SEQUENCE.
RC TISSUE=THORACIC GANGLION;
RX MEDLINE; 92196111.
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated callifamides) from the blowfly
RT Calliphora vomitoria";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; C41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TOP 4
Db :||
3 SQD 5

RESULT 29
NSK1_SARBU STANDARD; PRT; 9 AA.
AC P41492;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE NEOSULFAKININ-I (NEB-SK-I).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Sarcophagidae; Sarcophaga.
RN [1]
RP SEQUENCE.
RC TISSUE-HEAD;
RX MEDLINE; 93083101.
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: MYOTROPIC PEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PROSITE; PS00259; GASTRIN; 1.
KW Neuropeptide; Amidation; Sulfatation.
FT MOD_RES 4 4 SULFATATION (POTENTIAL).
FT MOD_RES 9 9 AMIDATION (POTENTIAL).
SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
Db :||
2 DD 3

RESULT 30
UHA2_HUMAN STANDARD; PRT; 9 AA.
ID P40929;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART (SPOT 5603) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]
RP SEQUENCE.
RC TISSUE=HEART;
RX MEDLINE; 95203287.
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994.";
RL Electrophoresis 15:1459-1465(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0, ITS MW IS: 55.3 KD.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1104 MW; 8874B1BB5B01B2CA CRC64;

Query Match 34.3%; Score 12; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DD 5
Db :||
8 DD 9

Search completed: June 30, 2000, 19:03:14
Job time: 15037 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:07:09 ; Search time 53.11 Seconds
(without alignments)

9.138 Million cell updates/sec

Title: US-08-833-506C-89

Perfect score: 35

Sequence: 1 VTQDDIQ 7

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

SPTREMBL12.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_prodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	57.1	12	4	Q13695 homo sapien
2	50	57.1	14	12	O84179 porcine ade
3	19	54.3	11	9	Q38415 bacteriophage
4	17	48.6	12	8	P92457 ephedra sp.
5	17	48.6	15	2	Q53541 bacillus sp
6	15	42.9	8	4	Q15893 homo sapien
7	15	42.9	9	11	O63924 mus musculus
8	15	42.9	11	2	Q47602 escherichia
9	15	42.9	14	11	Q921H4 mus musculus
10	15	42.9	15	4	Q08947 homo sapien
11	15	42.9	15	4	Q16387 homo sapien
12	14	40.0	8	2	P72279 rhodococcus
13	14	40.0	8	4	Q15902 homo sapien
14	14	40.0	8	5	Q94895 physarum po
15	14	40.0	11	5	Q23876 dictyostell
16	14	40.0	13	2	Q48357 escherichia
17	14	40.0	13	5	O61340 panulirus i
18	14	40.0	14	4	Q16118 homo sapien
19	14	40.0	14	12	P91578 choristoneu
20	14	40.0	15	2	O52640 pseudomonas

21	13	37.1	9	2	Q47556	Q47556 escherichia
22	13	37.1	9	12	O83622	O83622 murray vall
23	13	37.1	10	11	Q83056	Q83056 rattus norv
24	13	37.1	11	4	Q16427	Q16427 homo sapien
25	13	37.1	11	7	O78119	O78119 oreochromis
26	13	37.1	12	8	Q36622	Q36622 picea abies
27	13	37.1	12	8	Q36623	Q36623 picea abies
28	13	37.1	12	8	Q36668	Q36668 pinus sylve
29	13	37.1	12	8	Q36669	Q36669 pinus sylve
30	13	37.1	12	8	Q37791	Q37791 larix euroi
31	13	37.1	12	8	Q37790	Q37790 larix euroi
32	13	37.1	12	8	O03815	O03815 abies alba
33	13	37.1	12	8	O03816	O03816 metasequoia
34	13	37.1	12	8	O03817	O03817 taxus bacca
35	13	37.1	14	2	Q92842	Q92842 streptococc
36	13	37.1	15	10	O08936	O08936 nicotiana t
37	13	37.1	15	12	Q97090	Q97090 human immun
38	13	37.1	15	13	Q90403	Q90403 discopyge o
39	12	34.3	7	2	Q54248	Q54248 streptomyc
40	12	34.3	7	10	O49223	O49223 glycine max
41	12	34.3	9	12	Q70140	Q70140 human immun
42	12	34.3	10	2	P96305	P96305 alteromonas
43	12	34.3	10	2	P96423	P96423 pseudomonas
44	12	34.3	10	10	O08938	O08938 nicotiana t
45	12	34.3	11	2	Q52526	Q52526 plasmid sym
46	12	34.3	13	4	Q14461	Q14461 homo sapien
47	12	34.3	13	4	Q91674	Q91674 homo sapien
48	12	34.3	13	11	Q63047	Q63047 rattus norv
49	12	34.3	14	2	Q52093	Q52093 pigeon pea
50	12	34.3	14	4	P78359	P78359 homo sapien
51	12	34.3	14	4	Q16232	Q16232 homo sapien
52	12	34.3	14	5	Q26100	Q26100 pratylenchu
53	12	34.3	14	12	Q66201	Q66201 porcine tra
54	12	34.3	15	2	O68430	O68430 buchnera ap
55	12	34.3	15	2	Q54325	Q54325 staphylococ
56	12	34.3	15	10	O40562	O40562 nicotiana t
57	12	34.3	15	10	O40563	O40563 nicotiana t
58	12	34.3	15	11	Q92003	Q92003 rattus norv
59	12	34.3	15	12	Q97092	Q97092 human immun
60	12	34.3	15	12	Q97094	Q97094 human immun
61	11	31.4	8	2	Q921E9	Q921E9 neisseria m
62	11	31.4	9	12	O85710	O85710 rous sarcom
63	11	31.4	10	4	O60912	O60912 homo sapien
64	11	31.4	10	12	Q86580	Q86580 simian para
65	11	31.4	11	2	Q47600	Q47600 escherichia
66	11	31.4	11	2	Q47604	Q47604 escherichia
67	11	31.4	11	2	Q47569	Q47569 escherichia
68	11	31.4	11	12	P88018	P88018 human immun
69	11	31.4	11	13	Q90735	Q90735 gallus gall
70	11	31.4	13	2	Q50038	Q50038 mycobacteri
71	11	31.4	13	2	Q47601	Q47601 escherichia
72	11	31.4	13	4	Q15537	Q15537 homo sapien
73	11	31.4	13	5	Q24365	Q24365 drosophila
74	11	31.4	13	5	Q92422	Q92422 albinaria h
75	11	31.4	13	11	Q80517	Q80517 mus musculus
76	11	31.4	13	12	Q86129	Q86129 vesicular s
77	11	31.4	14	2	Q52840	Q52840 rhizobium l
78	11	31.4	14	2	Q921E1	Q921E1 acetobacter
79	11	31.4	14	2	Q921E1	Q921E1 campylobact
80	11	31.4	14	2	Q921E1	Q921E1 campylobact
81	11	31.4	14	12	Q84708	Q84708 porcine epi
82	11	31.4	15	2	O54298	O54298 salmonella
83	11	31.4	15	2	Q47892	Q47892 fremyella d
84	11	31.4	15	6	O46661	O46661 macropus ro
85	10	28.6	7	2	O07354	O07354 synchococc
86	10	28.6	7	11	O63480	O63480 rattus norv
87	10	28.6	8	2	O68485	O68485 klebsiella
88	10	28.6	8	4	Q15895	Q15895 homo sapien
89	10	28.6	8	5	O15899	O15899 babesia ovi
90	10	28.6	8	7	Q29810	Q29810 homo sapien
91	10	28.6	8	11	O61715	O61715 mus musculu
92	10	28.6	8	12	Q66807	Q66807 echovirus 2
93	10	28.6	9	2	Q45533	Q45533 bacillus su

O95953 homo sapien
Q9xjn0 bacterioph
Q85723 simian sarc
Q8612 middelburg
Q50032 mycobacteri
Q26093 pisaster oc
Q9xs84 equus cabal

94 10 28.6 9 4 O95953
95 10 28.6 9 9 O9XJN0
96 10 28.6 9 12 Q85723
97 10 28.6 9 12 Q8612
98 10 28.6 10 2 Q50032
99 10 28.6 10 5 Q26093
100 10 28.6 10 6 Q9XS84

ALIGNMENTS

RESULT 1
Q13695
ID Q13695 PRELIMINARY; PRT; 12 AA.
AC Q13695;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ACETYLCHOLINE RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-THYMUS;
RX MEDLINE; 94071933.
RA MIHOVILOVIC M., MAI Y., HERBSTREITH M., RUBBOLI F., TARRONI P.,
RA CLEMENTI F., ROSES A.D.;
RT "Splicing of an anti-sense Alu sequence generates a coding sequence
variant for the alpha-3 subunit of a neuronal acetylcholine
receptor.";
RL Biochem. Biophys. Res. Commun. 197:137-144(1993).
DR EMBL; L18973; AAA86792.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1282 MW; CF969363 CRC32;

Query Match 57.1%; Score 20; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDDLQ 7
|:::|
DB 6 VTONGVQ 12

RESULT 2
Q84179
ID Q84179 PRELIMINARY; PRT; 14 AA.
AC Q84179;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE PROTEINASE (FRAGMENT).
GN 23K.
OS Porcine adenovirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
RN [1]
RP SEQUENCE FROM N.A.
RA MCCOY R.J., JOHNSON M.A., SHEPPARD M.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34592; AAB02184.1; -.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1582 MW; 478FF81D CRC32;

Query Match 57.1%; Score 20; DB 12; Length 14;
Best Local Similarity 50.0%; Pred. No. 3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
|:::|

Db 4 TEDEL 9

RESULT 3
Q38415 PRELIMINARY; PRT; 11 AA.
ID Q38415;
AC Q38415;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ANT1 PROTEIN (FRAGMENT).
OS Bacteriophage P7.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90335968.
RA CITRON M., SCHUSTER H.;
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
RL Cell 62:591-598(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92319637.
RA CITRON M., SCHUSTER H.;
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
RNA.";
RL Nucleic Acids Res. 20:3085-3090(1992).
DR EMBL; M35139; AAA32437.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1315 MW; F2E5018A CRC32;

Query Match 54.3%; Score 19; DB 9; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDDL 6
|:::|
DB 6 VTRNDI 11

RESULT 4
P92457
ID P92457 PRELIMINARY; PRT; 12 AA.
AC P92457;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE
REDUCTASE (FRAGMENT).
GN CHLB GENE.
GN Ephedra sp.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphylliphytes; Spermatophyta; Gnecophyta; Gnecopsida; Ephedrales;
OC Ephedraceae; Ephedra.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97263785.
RA KARPINSKA B., KARPINSKI S., HALLGREN J.E.;
RT "The chlB gene encoding a subunit of light-independent
protochlorophyllide reductase is edited in chloroplasts of conifers.";
RL Curr. Genet. 31:343-347(1997).
DR EMBL; X98573; CAA67182.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1441 MW; B036E488 CRC32;

Query Match 48.6%; Score 17; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDQ 7
:|||
Db 1 EDQ 4

RESULT 5
ID Q53541 PRELIMINARY; PRT; 15 AA.
AC Q53541:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE ORF2 PROTEIN (FRAGMENT).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95400017.
RA SETO Y., HASHIMOTO M., USAMI R., HAMAMOTO T., KUDO T., HORIKOSHI K.;
RT "Characterization of a mutation responsible for an alkali-sensitive
RT mutant, 18224, of alkaliphilic Bacillus sp. strain C-125.";
RL Biosci. Biotechnol. Biochem. 59:1364-1366(1995).
DR EMBL; S79441; AAB35256.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1529 MW; B149434E CRC32;

Query Match 48.6%; Score 17; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
:|||
Db 10 IAEED 14

RESULT 6
ID Q15893 PRELIMINARY; PRT; 8 AA.
AC Q15893:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE (CLONE XP587A) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XIONG M.,
RA COOLBAUGH M.I., CHINAULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,
RA CASKEY C.T.H.;
RL Hum. Mol. Genet. 0:0-0(0).
DR EMBL; L32073; AAA73883.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 874 MW; 599EA97B CRC32;

Query Match 42.9%; Score 15; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQDDLQ 7
:|:|
Db 1 SQNPQ 6

RESULT 7
ID Q63924 PRELIMINARY; PRT; 9 AA.

AC Q63924:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE CAMP-RESPONSIVE ELEMENT MODULATOR (ALTERNATIVE PROMOTER) (FRAGMENT).
GN CREM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94073967.
RA MOLINA C.A., FOULKES N.S., LALLI E., SASSONE-CORSI P.;
RT "Inducibility and negative autoregulation of CREM: an alternative
RT promoter directs the expression of ICER, an early response
RT repressor.";
RL Cell 75:875-886(1993).
DR EMBL; S67785; CAB32857.1; -.
DR MGD; MGI:88495; Crem.
FT NON_TER 9
SQ SEQUENCE 9 AA; 880 MW; BA9D1365 CRC32;

Query Match 42.9%; Score 15; DB 11; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
:|||
Db 3 VTGDE 7

RESULT 8
ID Q47602 PRELIMINARY; PRT; 11 AA.
AC Q47602:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE C (FRAGMENT).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91139577.
RA TAO T., BOURNE J.C., BLUMENTHAL R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63620; AAA24558.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1412 MW; BC68F8F4 CRC32;

Query Match 42.9%; Score 15; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQDD 5
:||||
Db 1 MSRDD 5

RESULT 9
ID Q921H4 PRELIMINARY; PRT; 14 AA.
AC Q921H4:
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE B144 PROTEIN A (FRAGMENT).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88031493.
 RA TSUGE I., SHEN F.-W.W., STEINMETZ M., BOYSE E.A.;
 RT "A gene in the H-2S:H-2D interval of the major histocompatibility
 complex which is transcribed in B cells and macrophages.";
 RL Immunogenetics 26:378-380(1987).
 DR EMBL; M18187; AAA37272.1; -.
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1542 MW; 607F3593 CRC32;

Query Match 42.9%; Score 15; DB 11; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7
 Db 3 DLQ 5

RESULT 10
 Q08947 PRELIMINARY; PRT; 15 AA.
 AC Q08947;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
 DE DYSTROPHIN (DP1216) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93291881.
 RA BYERS T.J., LIDOV H.G., KUNKEL L.M.;
 RT "An alternative dystrophin transcript specific to peripheral nerve.";
 RL Nat. Genet. 4:77-81(1993).
 DR EMBL; S62617; AAB27159.1; -.
 KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
 KW Duplication; Alternative splicing.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1855 MW; AE9F9478 CRC32;

Query Match 42.9%; Score 15; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DLQ 7
 Db 11 DLQ 13

RESULT 11
 Q16387 PRELIMINARY; PRT; 15 AA.
 AC Q16387;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
 DE MEX40 PROTEIN (FRAGMENT).
 GN MEX40.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95400293.
 RA BUDARF M.L., COLLINS J., GONG W., ROE B., WANG Z., BAILEY L.C.,

RA SELLINGER B., MICHAUD D., DRISCOLL D.A., EMANUEL B.S.;
 RT "Cloning a balanced translocation associated with DiGeorge syndrome
 and identification of a disrupted candidate gene.";
 RL Nat. Genet. 10:269-278(1995).
 DR EMBL; S79494; AAD14302.1; -.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1626 MW; 746EEG2B CRC32;

Query Match 42.9%; Score 15; DB 4; Length 15;
 Best Local Similarity 60.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QDDLQ 7
 Db 10 RDGLQ 14

RESULT 12
 P72279 PRELIMINARY; PRT; 8 AA.
 AC P72279;
 DT 01-FEB-1997 (TEMBLrel. 02, Created)
 DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
 DE BIPHENYL DIOXYGENASE (FRAGMENT).
 GN BPHB.
 OS Rhodococcus globerulus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95255652.
 RA ASTURIAS J.A., DIAZ E., TIMMIS K.N.;
 RT "The evolutionary relationship of biphenyl dioxygenase from gram-
 positive Rhodococcus globerulus P6 to multicomponent dioxygenases from
 gram-negative bacteria.";
 RL Gene 156:11-18(1995).
 DR EMBL; X80041; CAA56350.1; -.
 KW Dioxygenase.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 989 MW; ED28AD0A CRC32;

Query Match 40.0%; Score 14; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.3e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 QDDL 6
 Db 4 QDEV 7

RESULT 13
 Q15902 PRELIMINARY; PRT; 8 AA.
 AC Q15902;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-AUG-1998 (TEMBLrel. 07, Last annotation update)
 DE (CLONE XP7E7A) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XIONG M.,
 RA COOLBAUGH M.I., CHINAULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,
 RA CASKEY C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0); -.
 DR EMBL; L32081; AAA73892.1; -.
 FT NON_TER 1

AC Q16118;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE CYCLIC ADENOSINE 3',5'-MONOPHOSPHATE RESPONSE ELEMENT BINDING PROTEIN
DE CREB [ALTERNATIVELY SPLICED, EXON W] (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94158910.
RA WAEBER G., MEYER T.E., LESIEUR M., HERMANN H.L., GERARD N.,
RA HABENER J.H.;
RT "Developmental stage-specific expression of cyclic adenosine 3',5'-
RT monophosphate response element binding protein CREB during
RT spermatogenesis involves alternative exon splicing.";
RL Mol. Endocrinol. 7:1501-1501(1993).
DR EMBL; S68577; AAB29985.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1698 MW; 86068950 CRC32;

Query Match 40.0%; Score 14; DB 4; Length 14;
Best Local Similarity 75.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQD 4
| |
Db 5 VKQD 8

RESULT 19
P91578
ID P91578 PRELIMINARY; PRT; 14 AA.
AC P91578;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE (FRAGMENT).
GN NPH 1.
OS Choriostaura fumiferana entomopoxvirus (CfEPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
RN [1]
RP SEQUENCE FROM N.A.
RA LI X., BARRETT J.W., YUEN L., ARIF B.M.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U19239; AAB39411.1; -.
KW Hydrolase.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1762 MW; 940E3C99 CRC32;

Query Match 40.0%; Score 14; DB 12; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.6e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQD 4
| |
Db 9 ITND 12

RESULT 20
O52640
ID O52640 PRELIMINARY; PRT; 15 AA.
AC O52640;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE NTNU (FRAGMENT).
GN NTNU.
OS Pseudomonas sp.

AC Q16118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TW3;
RX MEDLINE; 98215169.
RA JAMES K.D., WILLIAMS P.A.;
RT "ntn genes determining the early steps in the divergent catabolism of
RT 4-nitrotoluene and toluene in Pseudomonas sp. strain TW3.";
RL J. Bacteriol. 180:2043-2049(1998).
DR EMBL; AF043544; AAC38356.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1781 MW; FDD1B267 CRC32;

Query Match 40.0%; Score 14; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 QDDLQ 7
| | |
Db 8 QSQLQ 12

RESULT 21
Q47556
ID Q47556 PRELIMINARY; PRT; 9 AA.
AC Q47556;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ASPARTATE TRANSCARBAMOYLASE REGULATORY CHAIN (FRAGMENT).
GN PYRI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 82275057.
RA PAUZA C.D., KARELS M.J., NAVRE M., SCHACHMAN H.K.;
RT "Genes encoding Escherichia coli aspartate transcarbamoylase: the
RT pyrb-pyri operon.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
RN [2]
RP SEQUENCE OF 1-5 FROM N.A.
RX MEDLINE; 83195078.
RA HOOVER T.A., ROOF W.D., FOLTERMANN K.F., O'DONOVAN G.A., BENCINI D.A.,
RA WILD J.R.;
RT "Nucleotide sequence of the structural gene (pyrb) that encodes the
RT catalytic polypeptide of aspartate transcarbamoylase of Escherichia
RT coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
DR EMBL; J01670; AAA24475.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1085 MW; F794543D CRC32;

Query Match 37.1%; Score 13; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.3e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
| | |
Db 1 MTHDN 5

RESULT 22
Q83622
ID Q83622 PRELIMINARY; PRT; 9 AA.
AC Q83622;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL PROTEIN (FRAGMENT).

OS Murray valley encephalitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 88118912.
 RA HAHN C.S., HAHN Y.S., RICE C.M., LEE E., DALGARNO L., STRAUSS E.G.,
 RA STRAUSS J.H.;
 RT "Conserved elements in the 3' untranslated region of flavivirus RNAs
 RT and potential cyclization sequences.";
 RL J. Mol. Biol. 198;33-41(1987).
 DR EMBL; M35172; AAA66627.1; -.
 KW Hypothetical protein; Repeat.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1055 MW; 7EF99143 CRC32;

Query Match 37.1%; Score 13; DB 12; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.3e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
 DB 3 VSED 6

RESULT 23
 Q63056 PRELIMINARY; PRT; 10 AA.
 AC Q63056;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE RAT ASIALOGLYCOPROTEIN RECEPTOR (ASGP).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87026895.
 RA WATTS C.;
 RT "Isolation and expression of cDNA clones for a rat liver
 RT asialoglycoprotein receptor.";
 RL Biosci. Rep. 6:527-534(1986).
 DR EMBL; M21739; AAA40763.1; -.
 SQ SEQUENCE 10 AA; 1312 MW; 0908A0D9 CRC32;

Query Match 37.1%; Score 13; DB 11; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.3e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
 DB 1 MTKD 4

RESULT 24
 Q16427 PRELIMINARY; PRT; 11 AA.
 AC Q16427;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-MAY-1999 (TREMELREL. 10, Last annotation update)
 DE DYSTROPHIN PROTEIN (FRAGMENT).
 GN DYSTROPHIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96163501.
 RA HOLDER E., MAEDA M., BIES R.D.;

RT "Expression and regulation of the dystrophin Purkinje promoter in
 RT human skeletal muscle, heart, and brain.";
 RL Hum. Genet. 97:232-239(1996).
 DR EMBL; S81419; AADI4362.1; -.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1299 MW; AF0E38FF CRC32;

Query Match 37.1%; Score 13; DB 4; Length 11;
 Best Local Similarity 40.0%; Pred. No. 7e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
 DB 4 VSSDE 8

RESULT 25
 O78119 PRELIMINARY; PRT; 11 AA.
 AC O78119;
 DT 01-NOV-1998 (TREMELREL. 08, Created)
 DT 01-NOV-1998 (TREMELREL. 08, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE MHC CLASS II B LOCUS 1 (FRAGMENT).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 OC Perciformes; Labroidae; Cichlidae; Oreochromis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98315113.
 RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,
 RA SUELTSMANN H., FIGUEROA F., KLEIN J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc
 RT class II B loci.";
 RL Genetics 149:1527-1547(1998).
 DR EMBL; AF050017; AAC41356.1; -.
 KW MHC.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87026895.
 RA WATTS C.;
 RT "Isolation and expression of cDNA clones for a rat liver
 RT asialoglycoprotein receptor.";
 RL Biosci. Rep. 6:527-534(1986).
 DR EMBL; M21739; AAA40763.1; -.
 SQ SEQUENCE 10 AA; 1312 MW; 0908A0D9 CRC32;

Query Match 37.1%; Score 13; DB 7; Length 11;
 Best Local Similarity 60.0%; Pred. No. 7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VTQDD 5
 DB 7 VTRCD 11

RESULT 26
 Q36622 PRELIMINARY; PRT; 12 AA.
 AC Q36622;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1996 (TREMELREL. 01, Last annotation update)
 DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
 DE REDUCTASE (FRAGMENT).
 GN CHLB.
 OS Picea abies (Norway spruce) (Picea excelsa).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
 OC Picea.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96163501.
 RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
 RL Curr. Genet. 0:0-0(0).

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DR EMBL; X98685; CAA67242.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 75FC0606 CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 27
Q36623 PRELIMINARY; PRT; 12 AA.
AC Q36623;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Picea abies (Norway spruce) (Picea excelsa).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Picea.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98685; CAA67243.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1475 MW; 7337C4ED CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 28
Q36668 PRELIMINARY; PRT; 12 AA.
AC Q36668;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Pinus sylvestris (Scots pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98683; CAA67240.1; -.

DR EMBL; X98685; CAA67242.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 75FC0606 CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 29
Q36669 PRELIMINARY; PRT; 12 AA.
AC Q36669;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Pinus sylvestris (Scots pine).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98684; CAA67241.1; -.
KW Chloroplast. 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1475 MW; 7337C4ED CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
Db 1 EDLK 4

RESULT 30
Q37791 PRELIMINARY; PRT; 12 AA.
AC Q37791;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TReMBLrel. 01, Last annotation update)
DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
DE REDUCTASE (FRAGMENT).
GN CHLB.
OS Larix eurolepis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Larix.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COTYLEDONS;
RA KARPINSKA B., KARPINSKI S., HILGREN J.E.;
RL Curr. Genet. 0:0-0(0).
DR EMBL; X98686; CAA67244.1; -.
DR EMBL; X98681; CAA67239.1; -.

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DR EMBL; X98679; CAA67237.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1445 MW; 75FC0606 CRC32;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDLQ 7
: : :
Db 1 EDLK 4

Search completed: June 30, 2000, 16:18:45
Job time: 7896 sec

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